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FILE 'REGISTRY' ENTERED AT 07:50:49 ON 03 MAY 2001
L1 3 S AGCGGGTCTATTAGA/SQSN

L1 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2001 ACS
RN 316113-07-2 REGISTRY
CN GenBank AX057545 (9CI) (CA INDEX NAME)
SQL 15
MF Unspecified
CI MAN

L1 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2001 ACS
RN 314014-76-1 REGISTRY
CN DNA, d(A-G-C-G-G-G-T-C-T-A-T-T-A-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0077259 SEQID: 1 claimed DNA
SQL 15
MF Unspecified
CI MAN

REFERENCE 1: 134:52240

L1 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2001 ACS
RN 241115-49-1 REGISTRY
CN GenBank AQ774045 (9CI) (CA INDEX NAME)
SQL 446
MF Unspecified
CI MAN

FILE 'CAPLUS' ENTERED AT 07:55:43 ON 03 MAY 2001
L2 1 S L1

L2 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:900854 CAPLUS
DOCUMENT NUMBER: 134:52240
TITLE: Peptide nucleic acid probes targeting rRNA sequence and hybridization assay for wine spoiling Dekkera/Brettanomyces yeast detection
INVENTOR(S): Hyldig-Nielsen, Jens J.; O'Keefe, Heather P.; Stender, Henrik
PATENT ASSIGNEE(S): Boston Probes, Inc., USA
SOURCE: PCT Int. Appl., 53 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 2000077259	A1	20001221	WO 2000-US16273	20000614

W: JP
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.: US 1999-139212 P 19990615

AB This invention is related to novel peptide nucleic acid (PNA) probes, probe sets, methods and kits pertaining to the detection, identification and/or quantitation of yeasts and particularly Dekkera bruxellensis (a.k.a. Brettanomyces) responsible for wine spoilage. The PNA probes targeted to rRNA sequence, labeled with chromophores, fluorophores, spin labels, radioisotopes, enzymes, haptens, and chemiluminescent compds., and may be immobilized on a support, are suitable for in situ hybridization. Polymerase, alk. phosphatase, horseradish peroxidase, or soybean peroxidase may be conjugated to the probe. The probes, probe sets, methods and kits of this invention are particularly well suited for use in the anal. of yeast in wine, beer and liquor and in the monitoring of contamination of in-process product as well as the equipment and facilities used to manuf. product in wineries and breweries. Detection of Dekkera/Brettanomyces yeast by dot-blot hybridization anal. using fluorescein, hapten, or soybean peroxidase-labeled PNA probes targeted to yeast rRNA sequences, is described. Application of the method to the detection of Zygosaccharomyces bailii in white zinfandel wine, of Candida yeast species. PNA fluorescent in situ hybridization (FISH) for Brettanomyces (Dekkera bruxellensis) detection is also described.

IT **314014-76-1D**, PNA
RL: ARG (Analytical reagent use); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(base sequence for PNA probe; peptide nucleic acid probes targeting rRNA sequence and hybridization assay for wine spoiling Dekkera/Brettanomyces yeast detection)

REFERENCE COUNT: 8

REFERENCE(S):
(1) Amoco Corp; EP 0497464 A 1992 CAPLUS
(2) Dako, A; WO 9824933 A 1998 CAPLUS
(3) Gene Trak Systems; EP 0422872 A 1991 CAPLUS
(4) Gildea, B; TETRAHEDRON LETTERS 1998, V39(40), P7255 CAPLUS
(5) Ibeas, J; APPLIED AND ENVIRONMENTAL MICROBIOLOGY 1996, P998 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

FILE 'HOME' ENTERED AT 07:56:06 ON 03 MAY 2001

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03may01 07:00:50 User219783 Session D1703.1

SYSTEM:OS - DIALOG OneSearch
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File 370:Science 1996-1999/Jul W3
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File 444:New England Journal of Med. 1985-2001/Apr W5
(c) 2001 Mass. Med. Soc.
File 162:CAB HEALTH 1983-2001/Mar
(c) 2001 CAB INTERNATIONAL
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See Help News162 for details.
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Set	Items	Description

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Set	Items	Description
S1	505094	(YEAST? ? OR DEKKERA OR BRETTANOMYC? OR CANDIDA OR SACCHAR-OMYC? OR CLAVISPOR?)
S10	13381	S1(5N)(DETERM? OR DETECT? OR DET??)
S11	94	S10 AND (SITU(5N)(HYBRIDIS? OR HYBRIDIZ?))
S12	66	RD (unique items)

key terms

>>>No matching display code(s) found in file(s): 43, 65

Searcher : Shears 308-4994

12/3,AB/1 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

14651606 PASCAL No.: 00-0323488
Community analysis of bacterial biofilms in a simulated recirculating cooling-water system by fluorescent in *situ"** *hybridization"** with rRNA-targeted oligonucleotide probes
MACDONALD R; BROZEL V S
Laboratory for Biofilm Physiology, Department of Microbiology and Plant Pathology University of Pretoria, Pretoria, 0002, South Africa
Journal: Water research : (Oxford), 2000, 34 (9) 2439-2446
Language: English
An open recirculating cooling-water system feeding a modified Robbin's Device (MRD) with synthetic cooling water to simulate the environment of a recirculating industrial cooling-water system was set up. Both mild steel and Nylon coupons were inserted to sample biofilms at regular intervals. The community structure was determined by in *situ"** *hybridization"** using fluorescently labelled 16 S and 23 S rRNA-targeted oligonuclcotide probes specific for the beta-, gamma- and delta subclasses of the Proteobacteria, as well as probes specific for the genera Shewanella, Aeromonas and Pseudomonas. A Cy5 labelled eubacterial probe was used in conjunction with other probes to overcome the problems experienced with autofluorescence. Due to the weak fluorescent signals obtained, biofilm samples were treated with glucose, yeast extract and chloramphenicol before fixation, to allow the cell volume and ribosome count to increase while suppressing cell division. The predominant bacteria in biofilms in the recirculating cooling-water systems were found to be members of the beta Proteobacteria (ca 50% of total bacteria observed with EUB 338) and unidentified large cocci, whereas gamma Proteobacteria were only observed occasionally (ca 10% of total bacteria observed with EUB 338). At first no Pseudomonas were *detected"**, but after the glucose, *yeast"** extract and chloramphenicol treatment, ca 5% of the gamma Proteobacteria present were found to be Pseudomonas. Shewanella putrefaciens were present in low numbers (ca 10% of the gamma Proteobacteria present), although well distributed. We did not observe any sulphate-reducing bacteria or Aeromonas.

12/3,AB/2 (Item 2 from file: 144)
DIALOG(R)File 144:Pascal

13718796 PASCAL No.: 98-0410079
Fluorescence in *situ"** *hybridization"** analysis of 12;21

translocation in Japanese childhood acute lymphoblastic leukemia
EGUCHI-ISHIMAE M; EGUCHI M; TANAKA K; HAMAMOTO K; OHKI M; UEDA K; KAMADA N
Department of Cancer Cytogenetics, Research Institute for Radiation Biology and Medicine, Hiroshima University, 1-2-3 Kasumi, Minami-ku, Hiroshima 734-8553, Japan; Hiroshima Red Cross Hospital and Atomic Bomb Survivors Hospital, 1-9-6 Sendamachi, Naka-ku, Hiroshima 730-0052, Japan; National Cancer Institute of Japan, 5-1-1 Tsukiji, Chuou-ku, Tokyo 104-0045, Japan; Department of Pediatrics, Hiroshima University School of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima 734-8551, Japan
Journal: Japanese journal of cancer research, 1998, 89 (7) 783-788
Language: English
Fluorescence in *situ"** *hybridization"** (FISH) analysis was applied to *detect"** t(12;21) using two *yeast"** artificial chromosome probes and cosmid probes covering the TEL(ETV6) and the AML1 gene to clarify the incidence of abnormality of t(12;21) in Japanese childhood acute lymphoblastic leukemia (ALL). We detected seven TEL/AML1 fusion positive patients (9.5%), all of whom were diagnosed as B-lineage ALL, among 74 childhood ALL. On the other hand, no TEL/AML1 fusion positive patients were found among 37 adult ALL. The incidence among Japanese seemed to he lower than that among other nations. Of the seven patients with the TEL/AML1 fusion, five exhibited normal karyotype, one was t(8;12)(q11;p13), i(21q) and the remaining one exhibited a near-triploid karyotype in conventional G-banding. The FISH method clearly demonstrated that all patients with the TEL/AML1 fusion had subpopulations of leukemic cells with deletion of the normal TEL allele. which is significant for understanding the progression of leukemia with t(12;21).

12/3,AB/3 (Item 3 from file: 144)
DIALOG(R)File 144:Pascal

13296656 PASCAL No.: 98-0019884
*Detection"** and identification of *Candida"** species in experimentally infected tissue and human blood by rRNA-specific fluorescent in *situ"** *hybridization"**
LISCHEWSKI A; KRETSCHMAR M; HOF H; AMANN R; HACKER J; MORSCHHAEUSER J
Zentrum fuer Infektionsforschung, Universitaet Wuerzburg, 97070 Wuerzburg, Germany; Institut fuer Medizinische Mikrobiologie und Hygiene, Klinikum der Stadt Mannheim, 68135 Mannheim, Germany; Max-Planck-Institut fuer Marine Mikrobiologie, 28359 Bremen, Germany
Journal: Journal of clinical microbiology, 1997, 35 (11) 2943-2948
Language: English
Two 18S rRNA-targeted oligonucleotide probes specific for Candida albicans and *Candida"** parapsilosis were used to *detect"** and identify

by fluorescent in *situ"** *hybridization"** these medically important Candida species in deep organs of mice after experimental systemic infection. The C. albicans-specific probe detected fungal cells in kidney, spleen, and brain sections ofa mouse infected with C. albicans but not in a mouse infected with the closely related species C. parapsilosis. Conversely, the C. parapsilosis-specific probe detected fungal cells in the deep organs of a mouse infected with C. parapsilosis but not in the deep organs of a C. albicans-infected mouse. In addition, the C. albicans-specific probe was used to detect this species in human blood spiked with yeast cells by a lysis-filtration assay and subsequent fluorescent in *situ"** *hybridization"**. By this assay, as few as three yeast cells per 0.5 ml of blood were consistently detected. Our results demonstrate that fluorescent in *situ"** *hybridization"** with species-specific rRNA-targeted oligonucleotide probes provides a novel, culture-independent method for the sensitive *detection"** and identification of *Candida"** species in clinically relevant material.

12/3,AB/4 (Item 4 from file: 144)
DIALOG(R)File 144:Pascal

13165042 PASCAL No.: 97-0426801

A chromosome 14q11/TCR alpha / delta specific *yeast"** artificial chromosome improves the *detection"** rate and characterization of chromosome abnormalities in T-lymphoproliferative disorders

RACK K A; CORNELIS F; RADFORD-WEISS I; BERNHEIM A; HARRISON C J; HERMINE O; PRIEUR M; VEKEMANS M; MACINTYRE E A

Department of Hematology, Hopital Necker Enfants Malades, Paris, France; INSERM U358, Hopital Saint-Louis, Paris, France; Laboratoire de Cytogenetique, Hopital Necker Enfants Malades, Paris, France; Laboratoire de Cytogenetique, Institut Gustave Roussy, Paris, France; Paterson Institute Christie Hospital, Manchester, United Kingdom; CNRS URA 1461, Universite Rene Descartes, Paris, France

Journal: Blood, 1997, 90 (3) 1233-1240

Language: English

The rate of detection of chromosome abnormalities in T-cell proliferations is lower than that observed in B-cell malignancies. The former frequently involve the TCR alpha / delta locus at chromosome band 14q11. We have identified a YAC encompassing 70% of the TCR alpha / delta locus, which has been used as a fluorescence in *situ"** *hybridization"** probe to detect chromosome rearrangements involving 14q11, both at metaphase and within interphase nuclei, in patients with a variety of T-lymphoproliferative disorders. Its use allowed detection of previously unsuspected TCR alpha / delta rearrangements in 4/13 (30%) immature T-lineage acute leukemias, including two t(10;14) and 2 minor inversion

14s. It also clarified interpretation of complex chromosome 14 abnormalities in mature T-cell proliferations (T-prolymphocytic leukemia and ataxia telangiectasia). Use of this probe will aid the detection and characterization of abnormalities involving the TCR alpha / delta locus, particularly in cases with normal or complex karyotypes and in those proliferations for which mitoses are difficult to obtain.

12/3,AB/5 (Item 5 from file: 144)
DIALOG(R)File 144:Pascal

12774650 PASCAL No.: 96-0490580

Specific *detection"** of *Candida"** albicans and *Candida"** tropicalis by fluorescent in *situ"** *hybridization"** with an 18S rRNA-targeted oligonucleotide probe

LISCHEWSKI A; AMANN R I; HARMSEN D; MERKERT H; HACKER J; MORSHHAEUSER J

Zentrum fuer Infektionsforschung, Universitaet Wuerzburg, Roentgenring 11 , 97070 Wuerzburg, Germany; Lehrstuhl fuer Mikrobiologie, Technische Universitaet Muenchen, Arcisstrasse 16, 80290 Muenchen, Germany; Institut fuer Hygiene und Mikrobiologie, Universitaet Wuerzburg, Josef-Schneider-Strasse 2, Bau 17, 97080 Wuerzburg, Germany; Institut fuer Molekulare Infektionsbiologie, Universitaet Wuerzburg, Roentgenring 11, 97070 Wuerzburg, Germany

Journal: Microbiology : (Spencers Wood), 1996, 142 (p.10) 2731-2740

Language: English

In *situ"** *hybridization"** of whole cells with rRNA-targeted, fluorescently labelled oligonucleotide probes is a powerful method to specifically detect micro-organisms in their natural habitat without cultivation and subsequent identification by phenotypic characterization. To examine the use of this method for the specific *detection"** of pathogenic *Candida"** species, we have designed an oligonucleotide probe which binds to the 18S rRNA of C. albicans and C. tropicalis, the two most important pathogenic Candida species, and differentiates them from other clinically relevant species. After establishing suitable hybridization conditions, we confirmed the specificity of our probe O20 in RNA dot blot hybridizations with a series of reference strains and clinical isolates of medically important Candida species. All C. albicans and C tropicalis strains hybridized with the probe, whereas all strains of C. parapsilosis, C. glabrata, C. krusei, C. guilliermondii. C. kefyr and C. lusitaniae did not. When we used the fluorescently labelled probe O20 to specifically detect single cells of the two target species by in *situ"** *hybridization"**, both C. albicans and C. tropicalis reacted strongly with the probe and could be clearly differentiated from C. krusei and C. parapsilosis, although the latter organism contains only two nucleotide mismatches in the probe target region. This discrimination capacity was

also seen when mixed suspensions of C. albicans and C. parapsilosis were hybridized with the probe. After infection of a human endothelial cell line with C. albicans and C. krusei, C. albicans cells adhering to the endothelial cells were easily distinguishable from the C. krusei cells by fluorescent in *situ"** *hybridization"** with probe O20. In addition, germ tubes and hyphae of C. albicans were also efficiently labelled. The application of fluorescently labelled rRNA-targeted oligonucleotide probes therefore appears to be a valuable tool for the specific detection and identification of different members of the genus Candida, which does not require any cultivation.

12/3,AB/6 (Item 6 from file: 144)
DIALOG(R)File 144:Pascal

12276806 PASCAL No.: 95-0507455
Detection of 9p deletions in leukemia cell lines by interphase fluorescence in *situ"** *hybridization"** with YAC-derived probes
DREYLING M H; KOBAYASHI H; OLOPADE O I; LE BEAU M M; ROWLEY J D; BOHLANDER S K
Univ. Chicago, dep. medicine, sect. hematology/oncology, Chicago IL 60637, USA
Journal: Cancer genetics and cytogenetics, 1995, 83 (1) 46-55
Language: English
Hemizygous and homozygous deletions of the type I interferon gene cluster (IFN) have been detected in about 20% of acute lymphoblastic leukemias. A putative tumor suppressor gene (TSG) is thought to be located centromeric to the IFN cluster on chromosomal bands 9p21-22. We studied the accuracy of fluorescence in *situ"** *hybridization"** (FISH) for *detecting"** deletions in interphase cells using *yeast"** artificial chromosome (YAC) clones containing all or part of the IFN cluster. FISH probes were generated from YACs (320-1300 kb in size) by a sequence-independent amplification technique (SIA). Fifteen cell lines (nine T-ALL, three B-cell precursor ALL, one B-ALL, one AML, one CML-BC) that had been well characterized by conventional cytogenetic analysis and molecular techniques were analyzed. We were able to detect all numerical changes ofthe IFN cluster including homozygous and hemizygous deletions accurately and to define subclones of the cell lines. Moreover, in six cell lines we were able to identify subclones. In dilution experiments the detection thresholds for subpopulations with homozygous and hemizygous deletions were determined to be 5% and Z5%, respectively.

12/3,AB/7 (Item 7 from file: 144)
DIALOG(R)File 144:Pascal

10511863 PASCAL No.: 93-0021114
*Detection"** and characterizarion of chimeric' *yeast"** artificial chromosome clones by fluorescent in *situ"** suppression *hybridization"**
SELLERI L; EUBANKS J H; GIOVANNINI M; HERMANSON G G; ROMO A; DJABALI M; MAURER S; MCELLIGOTT D L; SMITH M W; EVANS G A
Salk inst. biological studies, cent. human genome res., molecular genetics lab., La Jolla CA 92037, USA
Journal: Genomics : (San Diego, CA), 1992, 14 (2) 536-541
Language: English

12/3,AB/8 (Item 8 from file: 144)
DIALOG(R)File 144:Pascal

09308566 PASCAL No.: 91-0098940
Flow cytometric *detection"** of *yeast"** by in *situ"** *hybridization"** with a fluorescent ribosomal RNA probe
BERTIN B; BROUX O; VAN HOEGAERDEN M
Inst. cochin genetique moleculaire, lab. immunopharmacologie moleculaire, Paris 75014, France
Journal: Journal of microbiological methods, 1990, 12 (1) 1-12
Language: English
An in *situ"** *hybridization"** procedure with a fluorescent RNA probe applied to *yeast"** *detection"** by flow cytometry is described. The signal obtained with yeast antisense rRNA probe was 30 times higher than the nonspecific signal obtained with a bacterial sense rRNA probe. The yeast-specific signal was not eliminated after posthybridization RNase treatment although it completely disappeared when cells were treated with RNase before hydridization, confirming that rRNA was the target. With appropriate probes, the procedure could be used also for *detection"** of specific *yeast"** populations

12/3,AB/9 (Item 9 from file: 144)
DIALOG(R)File 144:Pascal

09025302 PASCAL No.: 90-0193494
*Detection"** of specific RNA sequences in *yeast"** by in *situ"** colony *hybridization"**
IVANOV I; MIRONOVA R; PHILIPOVA D; VENKOV P
Bulgarian acad. sci., inst. molecular biology, Sofia 1113, Bulgaria
Journal: Yeast (Chichester West Sussex), 1990, 6 (1) 31-34
Language: English
In this paper we describe a modification of the RNA colony hybridization

method applicable for *detection"** of specific RNA sequences in *yeast"**

12/3,AB/10 (Item 1 from file: 266)
DIALOG(R)File 266:FEDRIP

00314488
IDENTIFYING NO.: 7R29GM51996-06 AGENCY CODE: CRISP
GENETIC AND MOLECULAR ANALYSIS OF CHROMOSOME STRUCTURE
PRINCIPAL INVESTIGATOR: KOSTRIKEN, RICHARD G
ADDRESS: MILLS COLLEGE 5000 MACARTHUR BLVD OAKLAND, CA 94613
PERFORMING ORG.: MILLS COLLEGE, OAKLAND, CALIFORNIA
SPONSORING ORG.: NATIONAL INSTITUTE OF GENERAL MEDICAL SCIENCES
FY : 2000
SUMMARY: DESCRIPTION: This application "Genetic and Molecular Analysis of Chromosome Structure" proposes research to begin to gain an understanding of the genetic basis and the dynamics of chromosome structure, including folding patterns which may change during the cell cycle. The directionality of yeast mating type switching provides the model system for this work. Mating type switching occurs when the information located at the distal silent HMR or HML locus is used in a gene conversion event that results in its insertion at the MAT locus. The switch is directional in that in a given case the HMR locus will be strongly favored, whereas in others the information in HML locus is used. It appears probable that the switch involves a pairing of the MAT locus region with either the HMR or HML locus, depending upon the directionality of the event. This may occur at a specific stage of the cell cycle when these regions of chromosome III could be paired in preparation for switching.

Two related, efficient screens for mutants has been designed that will allow identification of genes required for the directionality of mating type switch. For example, the insertion of the ADE2 gene into the HMR allows identification of mutational changes in the directionality of switches since it allow *detection"** by red/white sectoring of *yeast"** colonies. The hypothesis to be tested is that a set of yet unidentified directionality genes encode trans-acting proteins which are required for the precise directionality of mating type switching.

Once mutations are identified which result in obvious changes in the red/white sectoring, a number of screens will be employed to eliminate from further consideration trivial mutants which do not appear to be directly relevant to directionality. Mutants that pass these tests will then be sorted into complementation groups, and the genes so identified will be cloned and analyzed. The putative directionality genes will be sequenced, disrupted, mapped, are characterized, including looking for homologies or motifs by comparison with protein data bases.

The second goal is to employ a technique known as fluorescent in *situ"** *hybridization"** (FISH) to detect predicted intrachromosomal pairing of the MAT locus with HMR (or HML), and to determine whether such

specific pairing of regions of chromsome III occurs during particular stages in the cell cycle. Fluorescent probes which hybridize to segments closely linked to HML, HMR and MAT will be used. This technique has already been successfully employed to examine interchromosomal pairing and thus it is anticipated that it can readily be applied to intrachromosomal pairing of regions of chromosomes. The results of this study will test the hypothesis that switching (and the directionality of switching) depends upon specific pairing of the relevant regions.

12/3,AB/11 (Item 2 from file: 266)
DIALOG(R)File 266:FEDRIP

00312960
IDENTIFYING NO.: 5R01GM33998-16 AGENCY CODE: CRISP
NUCLEOCYTOPLASMIC TRANSPORT OF MRNA IN YEAST
PRINCIPAL INVESTIGATOR: COLE, CHARLES N, JR.
ADDRESS: DARTMOUTH MEDICAL SCHOOL 7200 VAIL BLDG, RM 413A HANOVER, NH 03755-3844
PERFORMING ORG.: DARTMOUTH COLLEGE, HANOVER, NEW HAMPSHIRE
SPONSORING ORG.: NATIONAL INSTITUTE OF GENERAL MEDICAL SCIENCES
FY : 2000
SUMMARY: The long term objective of this research project is to understand how eukaryotic messenger RNA molecules are moved from their sites of transcription within the nucleus to their sites of translation in the cytoplasm. Nucleocytoplasmic transport of mRNA is an essential function of the eukaryotic cell, and likely requires the structural and functional integrity of the nucleus, including the nucleoskeleton, nuclear envelope and nuclear pore complexes.

An analysis of this mRNA export process in the yeast, Saccharomyces cerevisiae, has been underway in this laboratory for approximately three years. An assay that permits the *detection"** of poly(A)+ RNA in *yeast"** cells by in *situ"** *hybridization"** was developed and used to screen temperature sensitive yeast strains. Genes that encode proteins that may be important for mRNA export have been identified by using this RNA localization assay to isolate a new class of yeast mutants (RAT mutants for Ribonucleic Acid Trafficking). We lack detailed knowledge of many aspects of mRNA trafficking. Therefore, it is probable that among the genes identified will be some that encode critical components of nuclear structures and the nuclear pore. Identifying and understanding the functions of these proteins is essential for understanding mRNA trafficking and is the fundamental goal of this research.

A combination of genetic, molecular biological, cytological and biochemical approaches is proposed to extend the initial studies on these genes, to investigate the roles in mRNA trafficking of the proteins they encode, and to identify other cellular components involved in mRNA trafficking. Four specific aims are proposed:

1) The initial characterization of the rat mutants will be completed. This includes cloning, mapping, and sequence analysis (if the gene has not previously been sequenced) of each RAT gene. mRNA localization defects in mutant strains will be confirmed by cell fractionation. RNA and protein synthesis and RNA processing will be analyzed in mutant strains at permissive temperature and at various times after a shift to the restrictive temperature. The protein product of each RAT gene will be localized with antibodies.

2) A limited number of genes and gene products will be chosen for further study. For these genes, additional ts alleles will be isolated and examined and proteins which interact with their gene products will be identified through use of the two hybrid protein-protein interaction system of S. Fields or through the isolation of extragenic suppressors.

3) The sensitivity of the mRNA localization assay will be increased so that individual mRNA species can be localized.

4) The effect on nucleocytoplasmic mRNA export of mutation in a number of other *yeast"** genes will be *determined"** by performing the in situ poly(A)+ RNA localization assay on additional mutant yeast strains.

12/3,AB/12 (Item 3 from file: 266)
DIALOG(R)File 266:FEDRIP

00304329
IDENTIFYING NO.: 5R01DK38558-12 AGENCY CODE: CRISP
MECHANISMS OF GLOMERULAR IMMUNE INJURY
PRINCIPAL INVESTIGATOR: SEDOR, JOHN R
ADDRESS: METROHEALTH MEDICAL CENTER 2500 METROHEALTH DRIVE CLEVELAND, OH 44109-1998
PERFORMING ORG.: CASE WESTERN RESERVE UNIVERSITY, CLEVELAND, OHIO
SPONSORING ORG.: NAT INST OF DIABETES AND DIGESTIVE AND KIDNEY DISEASES
FY : 2000

SUMMARY: The molecular characterization of human and experimental renal injury has resulted in two consistent insights. First the intrinsic population of kidney cells are not passive bystanders injured by infiltrating leukocytes. Rather resident cells become "activated" after injury and participate in the subsequent destructive and restorative processes that ensue. Second renal cells serve as a source and target of biological modifiers that mediate nephron injury and repair. Third extracellular matrix composition is modified. How these observation collaborate to induce tissue injury is not understood but definition of more proximate regulators of these events is necessary to effectively interrupt the pathogenic mechanisms that drive nephron destruction. Our laboratory has focused on the IL-1 activated mesangial cell in an effort to define molecular and cellular mechanisms of progressive renal disease. Our published and preliminary data demonstrate: 1) IL-1 induces specialized changes in MC structure and function inpart by induction of a specific gene

set; 2) MC cultured under standard conditions express an "activated" or inflammatory phenotype but when appropriately cultured retain a more in vivo-like phenotype; 3) proinflammatory mediators and matrix remodelling collaborate to transcriptionally activate an inflammatory MC phenotype. From these data, we hypothesize that a ECM-dependent change in cell shape is permissive for cytokine mediated changes in cell structure and function. This project fits into the broad experimental goals of our laboratory to molecularly define mechanisms of the cytokine-activated phenotype in vitro and to assess whether such a "defined' MC phenotype can be identified in vivo. We will test our hypothesis using three model systems; MC cultured on plastic; MC cultured on various substratum; and in an animal model of primary mesangial injury. We will specifically:

1. Define further the transmembrane signalling pathways activate by the IL-1-IL-1R interaction in MC cultured on plastic.

a. What kinases are activated: We will asses for change in phosphorylation state by immunoprecipitation and subsequent immunoblotting.

b. What proteins interact with the IL-1 receptor. Expression library screening and *yeast"** genetics.

II. *Determine"** how change i cell substratum interactions affect cell biology by assessing effects of proinflammatory mediators and matrix on a-smooth muscle expression as a model gene.

a. stress vs integrins

b. 5'-regulatory regions

III. To analyze changes in ECM gene expression and indicators of mesangial cell activation in a model of primary mesangial injury.

a. immunohistochemistry, in situ etc b. to change intraglomerular gene expression by in vivo gene transfer

12/3,AB/13 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts

03949623 CAB Accession Number: 20001007795

Brome mosaic virus RNA replication proteins 1a and 2a colocalize and 1a independently localizes on the yeast endoplasmic reticulum.

Restrepo-Hartwig, M.; Ahlquist, P.

Institute for Molecular Virology, University of Wisconsin-Madison, 1525 Linden Dr., Madison, WI 53706-1596, USA.

Journal of Virology vol. 73 (12): p.10303-10309

Publication Year: 1999

ISSN: 0022-538X --

Language: English

Document Type: Journal article

The universal membrane association of positive-strand RNA virus RNA replication complexes is implicated in their function, but the intracellular membranes used vary among viruses. Brome mosaic virus (BMV) encodes two mutually interacting RNA replication proteins: 1a, which

contains RNA capping and helicase-like domains, and the polymerase-like 2a protein. In cells from the natural plant hosts of BMV, 1a and 2a colocalize on the endoplasmic reticulum (ER). 1a and 2a also direct BMV RNA replication and subgenomic mRNA synthesis in the yeast Saccharomyces cerevisiae, but whether the distribution of 1a, 2a, and active replication complexes in yeast duplicates that in plant cells has not been *determined"**. For *yeast"** expressing 1a and 2a and replicating BMV genomic RNA3, we used double-label confocal immunofluorescence to define the localization of 1a, 2a, and viral RNA and to explore the determinants of replication complex targeting. As in plant cells, 1a and 2a colocalized on and were retained on the *yeast"** ER, with no *detectable"** accumulation in the Golgi apparatus. 1a and 2a were distributed over most of the ER surface, with strongest accumulation on the perinuclear ER. In vivo labeling with bromo-UTP showed that the sites of 1a and 2a accumulation were the sites of nascent viral RNA synthesis. In *situ"** *hybridization"** showed that completed viral RNA products accumulated predominantly in the immediate vicinity of replication complexes but that some, possibly more mature cells also accumulated substantial viral RNA in the surrounding cytoplasm distal to replication complexes. Additionally, we find that 1a localizes to the ER when expressed in the absence of other viral factors. These results show that BMV RNA replication in yeast duplicates the normal localization of replication complexes, reveal the intracellular distribution of RNA replication products, and show that 1a is at least partly responsible for the ER localization and retention of the RNA replication complex. 48 ref.

12/3,AB/14 (Item 2 from file: 50)
DIALOG(R)File 50:CAB Abstracts

03589841 CAB Accession Number: 980404136
Rapid *detection"** and identification of *yeasts"** in yoghurt using fluorescently labelled oligonucleotide probes.
Kosse, D.; Ostenrieder, I.; Seiler, H.; Scherer, S.
Institut fur Mikrobiologie, Forschungszentrum fur Milch und Lebensmittel, Technische Universitat Munchen, Vottingerstr. 45, D-85354 Freising-Weihenstephan, Germany.
Yeasts in the dairy industry: positive and negative aspects. Proceedings, Copenhagen, Denmark, 2-3 September 1996.
Conference Title: Yeasts in the dairy industry: positive and negative aspects. Proceedings, Copenhagen, Denmark, 2-3 September 1996.
p.132-137
Publication Year: 1998
Publisher: International Dairy Federation -- Brussels, Belgium
ISBN: 92-9098-027-X
Language: English
Document Type: Conference paper

18S ribosomal RNA-targeted oligonucleotide probes were designed for the rapid and reliable identification of the dominant spoilage yeasts Candida parapsilosis, C. glabrata (Torulopsis glabrata), Clavispora lusitaniae, Debaryomyces hansenii, Dekkera bruxellensis, Hanseniaspora uvarum, Pichia anomala, P. membranaefaciens, Rhodotorula glutinis and Saccharomyces cerevisiae in milk products. In situ identification of S. cerevisiae, P. anomala, D. bruxellensis and D. hansenii in pure culture with species-specific fluorescently labelled oligonucleotides yielded strong fluorescent signals. S. cerevisiae and P. anomala were successfully detected in artificially-contaminated yoghurt using corresponding species-specific fluorescently-labelled probes in pure culture and in mixed culture assays. Isolates of P. anomala and S. cerevisiae from dairies also yielded strong fluorescent signals. The practical *detection"** limit of *yeasts"** by in *situ"** *hybridization"** was 103 c.f.u./g yoghurt. *Detection"** and identification of *yeasts"** from a spoiled yoghurt sample can be performed within 10 h. Dot-blot hybridization analyses with digoxigenin-labelled specific probes can be used in case of a limited accessibility of potential target sites on 18S ribosomal RNA during in *situ"** *hybridization"**. Identification by microtitre plates, dot-blot *hybridization"**, in *situ"** *hybridization"** and Fourier transform infrared spectroscopy are compared. 12 ref.

12/3,AB/15 (Item 3 from file: 50)
DIALOG(R)File 50:CAB Abstracts

03458382 CAB Accession Number: 970404724
Test-in-Time microbiology.
Original Title: Test-in-Time Mikrobiologie.
Kohler, E.; Schonknecht, U.
Fa. Chemunex, Hindenburgstrasse 44, D-73728 Esslingen, Germany.
DMZ, Lebensmittelindustrie und Milchwirtschaft vol. 117 (18): p.870-872
Publication Year: 1996
ISSN: 0938-9369 --
Language: German
Document Type: Journal article
ChemFlow' and 'ChemScan' fluorimetry and flow cytometry equipment is presented. The former is used for *detecting"** mould and *yeast"** contamination in yoghurt and for *determining"** total cell counts and product life of samples. The latter is used for detecting microorganisms in filtrates on membrane filter surfaces. For *detection"** of moulds and *yeasts"** , a non-fluorescent substrate of cell enzymes is split after entry into the cell and free fluorescein is formed. On injection into a flow cuvette, a laser causes each individual cell to fluoresce. This fluorescence is measured and evaluated, and individual contaminant cells

can be detected. Marking, incubation, filtration and measurement procedures are largely automated. Processing rates of 50 samples/h can be obtained. The use of 'ChemFlow' in determining product life is also discussed, as is its use in determining total viable cell counts in 1 ml pasteurized milk samples. 'ChemScan' equipment can analyse filtrates which have not been enriched using Fluorescence In-*situ"** *Hybridization"**. An oscillating laser scanner detects single fluorescence marked cells on membrane filter surfaces, validates them, and localizes them on a scan map. Through identification and discrimination of smoke effects, a sensitivity of 1 cell/membrane filter surface can be achieved. The sample is filtered through a 0.22 or 0.45 micro m membrane. Marking of the microorganism takes place over a 30 min period at 30 deg C, directly on the filter. Marking of cells specific to particular microorganisms is at a developmental stage. In less than or equal to 2 min the entire membrane surface can be scanned, and visual confirmation of results obtained with an attached fluorescence microscope.

12/3,AB/16 (Item 4 from file: 50)
DIALOG(R)File 50:CAB Abstracts

02908414 CAB Accession Number: 941201839
The effects of human immunodeficiency virus infection on macrophage phagocytosis of Candida.
Eversole, L. R.; Fleischmann, J.; Baldwin, G. C.; Sapp, J. P.
Section of Diagnostic Sciences, UCLA School of Dentistry, Los Angeles, CA 90024, USA.
Oral Microbiology and Immunology vol. 9 (1): p.55-59
Publication Year: 1994
ISSN: 0902-0055 --
Language: English
Document Type: Journal article
The effects of HIV infection on the phagocytic function towards C. pseudotropicalis (C. kefyr) were tested using monocytotropic and non-monocytotropic HIV strs. on peripheral blood monocytes. There were no differences in quantitative phagocytic activity or efficacy between the 2 infected and control mock-infected monocytes. Immunofluorescence for cytoplasmic p24 antigen and in *situ"** *hybridization"** for detection of HIV-specific RNA sequences revealed that few cells (10-4) showed productive infection. Occasional cells with active infection as defined by microscopically *detectable"** fluorescence labelling contained phagocytized *yeasts"**. 22 ref.

12/3,AB/17 (Item 5 from file: 50)
DIALOG(R)File 50:CAB Abstracts

02877841 CAB Accession Number: 940104726

Murine cerebellar neurons express a novel gene encoding a protein related to cell cycle control and cell fate determination proteins.

Taoka, M.; Isobe, T.; Okuyama, T.; Watanabe, M.; Kondo, H.; Yamakawa, Y. ; Ozawa, F.; Hishinuma, F.; Kubota, M.; Minegishi, A.; Song, S. Y.; Yamakuni, T.

Department of Neuroscience, Mitsubishi Kasei Institute of Life Sciences, Machida, Tokyo 194, Japan.

Journal of Biological Chemistry vol. 269 (13): p.9946-9951

Publication Year: 1994

ISSN: 0021-9258 --

Language: English

Document Type: Journal article

cDNA for a novel protein (designated V-1) from rat cerebellum was isolated and sequenced (GenBank/EMBL accession number D26179). The encoded protein consisted of 117 amino acids, and contained 2.5 contiguous repeats of the cdc10/SW16 motif, which was originally found in the products of the cell cycle control genes of *yeasts"** and the cell fate *determination"** genes in Drosophila and Caenorhabditis elegans. In *situ"** *hybridization"** histochemistry revealed that the expression of the V-1 gene is transiently increased in postmigratory granule cells during postnatal rat cerebellar development, and thereafter is markedly suppressed, whereas Purkinje cells constitutively express V-1 mRNA. In contrast, cerebellar granule cells of staggerer mutant mice continued to express the V-1 gene even when the granule cells of normal mice have ceased to express it. It is suggested that the V-1 protein has a potential role in the differentiation of granule cells. 41 ref.

12/3,AB/18 (Item 1 from file: 149)

DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01789551 SUPPLIER NUMBER: 21048729 (USE FORMAT 7 OR 9 FOR FULL TEXT)

Beta-cell transcription factors and diabetes: mutations in the coding region of the BETA2/NeuroD1 (NEUROD1) and Nkx2.2 (NKX2B) genes are not associated with maturity-onset diabetes of the young in Japanese.

Furata, Hiroto; Horikawa, Yukio; Iwasaki, Naoko; Hara, Manami; Sussel, Lori ; Le Beau, Michelle M.; Davis, Elizabeth M.; Ogata, Makiko; Iwamoto, Yasuhiko; German, Michael S.; Bell, Graeme I.

Diabetes, v47, n8, p1356(3)

August,

1998

PUBLICATION FORMAT: Magazine/Journal; Refereed ISSN: 0012-1797

LANGUAGE: English RECORD TYPE: Fulltext TARGET AUDIENCE: Professional

WORD COUNT: 3033 LINE COUNT: 00253

12/3,AB/19 (Item 2 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01487416 SUPPLIER NUMBER: 15673882 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Esophageal disease in human immunodeficiency virus infection.
Laine, Loren; Bonacini, Maurizio
Archives of Internal Medicine, v154, n14, p1577(6)
July 25,
1994
PUBLICATION FORMAT: Magazine/Journal ISSN: 0003-9926 LANGUAGE: English
RECORD TYPE: Fulltext; Abstract TARGET AUDIENCE: Professional
WORD COUNT: 4032 LINE COUNT: 00347

AUTHOR ABSTRACT: Up to 40% of patients with the acquired immunodeficiency syndrome may develop symptoms of esophageal disease. Candida esophagitis is responsible for the majority of the cases of esophageal disease; cytomegalovirus, herpes simplex, idiopathic esophageal ulcers, and Kaposi's sarcoma account for most of the remaining cases. Although endoscopy with esophageal biopsy and brushing is the gold standard for the diagnosis of esophageal disease in the acquired immunodeficiency syndrome, we generally recommend initial empiric therapy with an antifungal agent in patients with esophageal symptoms. Since effective treatment is available for most cases of esophageal disease in the acquired immunodeficiency syndrome, we recommend endoscopic evaluation in patients who do not respond to empiric therapy within 1 to 2 weeks. (Arch Intern Med. 1994;154:1577-1582)

12/3,AB/20 (Item 3 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01428452 SUPPLIER NUMBER: 14547809 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Ordered restriction maps of saccharomyces cerevisiae chromosomes constructed by optical mapping.
Schwartz, David C.; Li, Xiaojun; Hernandez, Luis I.; Ramnarain, Satyadarshan P.; Huff, Edward J.; Wang, Yu-Ker
Science, v262, n5130, p110(5)
Oct 1,
1993
PUBLICATION FORMAT: Magazine/Journal ISSN: 0036-8075 LANGUAGE: English
RECORD TYPE: Fulltext; Abstract TARGET AUDIENCE: Academic
WORD COUNT: 4184 LINE COUNT: 00346

AUTHOR ABSTRACT: A light microscope-based technique for rapidly constructing ordered physical maps of chromosomes has been developed. Restriction enzyme digestion of elongated individual DNA molecules (about

0.2 to 1.0 megabases in size) was imaged by fluorescence microscopy after fixation in agarose gel. The size of the resulting individual restriction fragments was determined by relative fluorescence intensity and apparent molecular contour length. Ordered restriction maps were then created from genomic DNA without reliance on cloned or amplified sequences for hybridization or analytical gel electrophoresis. Initial application of optical mapping is described for Saccharomyces cerevisiae chromosomes.

12/3,AB/21 (Item 4 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01193059 SUPPLIER NUMBER: 08177415 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Mapping the drosophila genome with yeast artificial chromosomes.
Garza, Dan; Ajioka, James W.; Burke, David T.; Hartl, Daniel L.
Science, v246, n4930, p641(6)
Nov 3,
1989
PUBLICATION FORMAT: Magazine/Journal ISSN: 0036-8075 LANGUAGE: English
RECORD TYPE: Fulltext TARGET AUDIENCE: Academic
WORD COUNT: 3991 LINE COUNT: 00363

12/3,AB/22 (Item 5 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01057468 SUPPLIER NUMBER: 02665462 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Gordon Research Conferences. (includes schedules) (calendar)
Science, v219, p1095(35)
March 4,
1983
DOCUMENT TYPE: calendar PUBLICATION FORMAT: Magazine/Journal ISSN:
0036-8075 LANGUAGE: English RECORD TYPE: Fulltext TARGET AUDIENCE:
Academic
WORD COUNT: 26464 LINE COUNT: 03173

12/3,AB/23 (Item 1 from file: 484)
DIALOG(R)File 484:Periodical Abstracts Plustext

04165633 (USE FORMAT 7 OR 9 FOR FULLTEXT)
The HIV-1 rev protein
Pollard, Victoria W; Malim, Michael H
Annual Review of Microbiology (IARM), v52, p491-532, p.42
1998

ISSN: 0066-4227 JOURNAL CODE: IARM
DOCUMENT TYPE: Feature
LANGUAGE: English RECORD TYPE: Fulltext; Abstract
WORD COUNT: 18223

ABSTRACT: The nuclear export of intron-containing HIV-1 RNA is critically dependent on the activity of Rev, a virally encoded sequence-specific RNA-binding protein. Rev shuttles between the nucleus and the cytoplasm and harbors both a nuclear localization signal and a nuclear export signal.

12/3,AB/24 (Item 2 from file: 484)
DIALOG(R)File 484:Periodical Abstracts Plustext

03394425 (USE FORMAT 7 OR 9 FOR FULLTEXT)
Dynamic molecular combing: Stretching the whole human genome for high-resolution studies
Michalet, Xavier; Ekong, Rosemary; Rousseaux, Sophie; et al
Science (GSCI), v277 n5331, p1518-1523, p.6
Sep 5, 1997
ISSN: 0036-8075 JOURNAL CODE: GSCI
DOCUMENT TYPE: Feature
LANGUAGE: English RECORD TYPE: Fulltext; Abstract
WORD COUNT: 4840

ABSTRACT: DNA in amounts representative of hundreds of eukaryotic genomes was extended on silanized surfaces by dynamic molecular combing.

12/3,AB/25 (Item 3 from file: 484)
DIALOG(R)File 484:Periodical Abstracts Plustext

03335873 (USE FORMAT 7 OR 9 FOR FULLTEXT)
Mitosis in living budding yeast: Anaphase a but no metaphase plate
Straight, Aaron F; Marshall, Wallace F; Sedat, John W; Murray, Andrew W
Science (GSCI), v277 n5325, p574-578, p.5
Jul 25, 1997
ISSN: 0036-8075 JOURNAL CODE: GSCI
DOCUMENT TYPE: Feature
LANGUAGE: English RECORD TYPE: Fulltext; Abstract
WORD COUNT: 3084

ABSTRACT: Chromosome movements and spindle dynamics were visualized in living cells of the budding yeast Saccharomyces cerevisiae.

12/3,AB/26 (Item 4 from file: 484)
DIALOG(R)File 484:Periodical Abstracts Plustext

03092900 (USE FORMAT 7 OR 9 FOR FULLTEXT)
Myc and Max homologs in drosophila
Gallant, Peter; Shiio, Yuzuru; Cheng, Pei Feng; Parkhurst, Susan M; Eisenman, Robert N
Science (GSCI), v274 n5292, p1523-1527, p.5
Nov 29, 1996
ISSN: 0036-8075 JOURNAL CODE: GSCI
DOCUMENT TYPE: Feature
LANGUAGE: English RECORD TYPE: Fulltext; Abstract
WORD COUNT: 3882

ABSTRACT: Homologs of the myc and max genes were cloned from the fruit fly Drosophila melanogaster and their protein products were shown to heterodimerize, recognize the same DNA sequence as their vetebrate homologs and activate transcription.

12/3,AB/27 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

134052240 CA: 134(5)52240h PATENT
Peptide nucleic acid probes targeting rRNA sequence and hybridization assay for wine spoiling Dekkera/Brettanomyces yeast detection
INVENTOR(AUTHOR): Hyldig-Nielsen, Jens J.; O'Keefe, Heather P.; Stender, Henrik
LOCATION: USA
ASSIGNEE: Boston Probes, Inc.
PATENT: PCT International ; WO 200077259 A1 DATE: 20001221
APPLICATION: WO 2000US16273 (20000614) *US PV139212 (19990615)
PAGES: 53 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A
DESIGNATED COUNTRIES: JP DESIGNATED REGIONAL: AT; BE; CH; CY; DE; DK; ES ; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE

12/3,AB/28 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

132290769 CA: 132(22)290769r PATENT
Detection of foreign microorganism using Snz and Sno genes and proteins as probes
INVENTOR(AUTHOR): Werner-Washburne, Margaret C.; Padilla, Pamela; Fuge, Edwina; Braun, Edward

LOCATION: USA
ASSIGNEE: University of New Mexico
PATENT: PCT International ; WO 200022169 A1 DATE: 20000420
APPLICATION: WO 99US23596 (19991008) *US PV103599 (19981009)
PAGES: 43 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A; H01L-021/20B; C07H-021/04B DESIGNATED COUNTRIES: AE; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CR; CU; CZ; DE; DK; DM; EE; ES; FI; GB; GD; GE; GH; GM; HR; HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; TZ; UA; UG; US; UZ; VN; YU; ZA; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW; SD; SL; SZ; TZ ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

12/3,AB/29 (Item 3 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

131017494 CA: 131(2)17494k PATENT
C-terminal BRCA1 interacting protein involved in cancer predisposition
INVENTOR(AUTHOR): Wong, Alexander K. C.; Bartel, Paul L.; Teng, David H. F.; Tavtigian, Sean V.
LOCATION: USA
ASSIGNEE: Myriad Genetics, Inc.
PATENT: PCT International ; WO 9927075 A1 DATE: 19990603
APPLICATION: WO 98US24831 (19981120) *US 975703 (19971121)
PAGES: 93 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-005/00A; C12N-015/63B; C12N-015/79B; C12N-015/11B; C12N-015/09B; C12N-005/10B
DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; HR; HU; ID; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; UZ; VN; YU; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW ; SD; SZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

12/3,AB/30 (Item 4 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

130220164 CA: 130(17)220164z PATENT
Rapid detection and identification of microorganisms by cell wall or membrane degradation and reaction with probes
INVENTOR(AUTHOR): Schut, Frederik; Tan, Paris Som Twan
LOCATION: Neth.
ASSIGNEE: Microscreen B.V.

PATENT: PCT International ; WO 9910533 A1 DATE: 19990304
APPLICATION: WO 98NL481 (19980826)
PAGES: 70 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A; G01N-033/569B; C07H-021/00B DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; HR; HU; ID; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM
DESIGNATED REGIONAL: GH; GM; KE; LS; MW; SD; SZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; GW; ML; MR; NE; SN; TD; TG

12/3,AB/31 (Item 5 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

128203678 CA: 128(17)203678m JOURNAL
Detection of bcr gene rearrangement in chronic myeloid leukemia by fluorescence in situ hybridization
AUTHOR(S): Liu, Mengmin; Liu, Xiaoli; Niu, Chao; He, Kaili; Xu, Xinyun; Cao, Qi; Chen, Zu; Chen, Saijuan
LOCATION: Shanghai Institute of Hematology, Ruijin Hospital, Shanghai Second Medical University, Shanghai, Peop. Rep. China, 200025
JOURNAL: Zhonghua Xueyexue Zazhi DATE: 1997 VOLUME: 18 NUMBER: 6
PAGES: 308-310 CODEN: CHTCD7 ISSN: 0253-2727 LANGUAGE: Chinese
PUBLISHER: Zhongguo Yixue Kexueyuan Xueyexue Yanjiuso

12/3,AB/32 (Item 6 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

128000948 CA: 128(1)948b PATENT
Method for simultaneous detection of multiple fluorophores for in situ hybridization and chromosome analysis
INVENTOR(AUTHOR): Garini, Yuval; Cabib, Dario; Buckwald, Robert A.; Soenksen, Dirk G.; Ried, Thomas
LOCATION: Israel
ASSIGNEE: Applied Spectral Imaging Ltd.; Garini, Yuval; Cabib, Dario; Buckwald, Robert A.; Soenksen, Dirk G.; Ried, Thomas
PATENT: PCT International ; WO 9740191 A1 DATE: 19971030
APPLICATION: WO 97US6225 (19970416) *US 635820 (19960422)
PAGES: 113 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A; G02B-021/00B DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GE; HU; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU; AM; AZ;

BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; KE; LS; MW; SD; SZ; UG ; AT; BE; CH; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; ML; MR; NE; SN; TD; TG

12/3,AB/33 (Item 7 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

127186242 CA: 127(14)186242z JOURNAL
A chromosome 14q11/TCR.alpha./.delta. specific yeast artificial chromosome improves the detection rate and characterization of chromosome abnormalities in L-lymphoproliferative disorders
AUTHOR(S): Rack, K. A.; Cornelis, F.; Radford-Weiss, I.; Bernheim, A.; harrison, C. J.; Hermine, O.; Prieur, M.; Vekemans, M.; Macintyre, E. A.
LOCATION: Dep. Hematol., Hop. Necker Enfants malades, Paris, Fr.
JOURNAL: Blood DATE: 1997 VOLUME: 90 NUMBER: 3 PAGES: 1233-1240
CODEN: BLOOAW ISSN: 0006-4971 LANGUAGE: English PUBLISHER: Saunders

12/3,AB/34 (Item 8 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

123247788 CA: 123(19)247788y JOURNAL
Translocations and amplification of the BCL2 gene are detected in interphase nuclei of non-Hodgkin's lymphoma by in situ hybridization with yeast artificial chromosome clones
AUTHOR(S): Taniwaki, Masafumi; Silverman, Gary A.; Nishida, Kazuhiro; Horike, Shigeo; Misawa, Shinichi; Shimazaki, Chihiro; Mura, Ikuo; Nagai, Masami; Abe, Masafumi; et al.
LOCATION: Third Dep. Internal Medicine, Kyoto Prefectural Univ. Medicine, Kyoto, Japan,
JOURNAL: Blood DATE: 1995 VOLUME: 86 NUMBER: 4 PAGES: 1481-6 CODEN: BLOOAW ISSN: 0006-4971 LANGUAGE: English

12/3,AB/35 (Item 9 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

120237580 CA: 120(19)237580y PATENT
Rapid detection of nucleic acids in stained specimens
INVENTOR(AUTHOR): Weber, William Dugald; Bresser, Joel; Blick, Mark; Ju, Shyhchen; Cubbage, Michael Lee; Asgari, Morteza
LOCATION: USA
ASSIGNEE: Research Development Foundation
PATENT: PCT International ; WO 9402645 A1 DATE: 940203

APPLICATION: WO 93US6732 (930716) *US 916779 (920717)
PAGES: 54 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A; C07H-021/04B DESIGNATED COUNTRIES: AU; CA; FI; JP; KR; NO; NZ; RU
DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE

12/3,AB/36 (Item 10 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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118161873 CA: 118(17)161873g JOURNAL
Detection and characterization of "chimeric" yeast artificial chromosome clones by fluorescent in situ suppression hybridization
AUTHOR(S): Selleri, Licia; Eubanks, James H.; Giovannini, Marco; Hermanson, Gary G.; Romo, Anthony; Djabali, Malek; Maurer, Susanne; McElligott, David L.; Smith, Michael W.; Evans, Glen A.
LOCATION: Mol. Genet. Lab., Salk Inst. Biol. Stud., La Jolla, CA, 92037, USA
JOURNAL: Genomics DATE: 1992 VOLUME: 14 NUMBER: 2 PAGES: 536-41
CODEN: GNMCEP ISSN: 0888-7543 LANGUAGE: English

12/3,AB/37 (Item 11 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

118141162 CA: 118(15)141162w PATENT
Rapid microbial diagnostics by in situ hybridization in aqueous suspension
INVENTOR(AUTHOR): Mueller, Uwe Richard; Cruickshank, Kenneth Alexander
LOCATION: USA
ASSIGNEE: Amoco Corp.
PATENT: European Pat. Appl. ; EP 497464 A1 DATE: 920805
APPLICATION: EP 92300344 (920115) *US 649569 (910131)
PAGES: 41 pp. CODEN: EPXXDW LANGUAGE: English CLASS: C12Q-001/68A; C12Q-001/70B; C12Q-001/06B DESIGNATED COUNTRIES: DE; FR; GB; IT; NL

12/3,AB/38 (Item 12 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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85073664 CA: 85(11)73664j JOURNAL
Isolation of bacteriophage .lambda. containing yeast ribosomal RNA genes: screening by in situ RNA hybridization to plaques
AUTHOR(S): Kramer, Richard A.; Cameron, John R.; Davis, Ronald W.
LOCATION: Sch. Med., Stanford Univ., Stanford, Calif.

JOURNAL: Cell DATE: 1976 VOLUME: 8 NUMBER: 2 PAGES: 227-32 CODEN: CELLB5 LANGUAGE: English

12/3,AB/39 (Item 1 from file: 156)
DIALOG(R)File 156:Toxline(R)

03835828 Subfile: TOXBIB-20-267872
Centromere clustering is a major *determinant"** of *yeast"** interphase nuclear organization.
Jin QW; Fuchs J; Loidl J
Institute of Botany, University of Vienna, Rennweg 14, A-1030 Vienna, Austria.
Source: J Cell Sci; VOL 113 (Pt 11), 2000, P1903-12 ISSN: 0021-9533 Coden: HNK
Language: ENGLISH
Document Type: JOURNAL ARTICLE
During interphase in the budding yeast, Saccharomyces cerevisiae, centromeres are clustered near one pole of the nucleus as a rosette with the spindle pole body at its hub. Opposite to the centromeric pole is the nucleolus. Chromosome arms extend outwards from the centromeric pole and are preferentially directed towards the opposite pole. Centromere clustering is reduced by the ndc10 mutation, which affects a kinetochore protein, and by the microtubule poison nocodazole. This suggests that clustering is actively maintained or enforced by the association of centromeres with microtubules throughout interphase. Unlike the Rabl-orientation known from many higher eukaryotes, centromere clustering in yeast is not only a relic of anaphase chromosome polarization, because it can be reconstituted without the passage of cells through anaphase. Within the rosette, homologous centromeres are not arranged in a particular order that would suggest somatic pairing or genome separation.

12/3,AB/40 (Item 2 from file: 156)
DIALOG(R)File 156:Toxline(R)

03588663 Subfile: TOXBIB-99-005237
Suppression of rho0 lethality by mitochondrial ATP synthase F1 mutations in Kluyveromyces lactis occurs in the absence of F0.
Chen XJ; Hansbro PM; Clark-Walker GD
Molecular and Cellular Genetics Group, Research School of Biological Sciences, The Australian National University, Canberra, ACT.
Source: Mol Gen Genet; VOL 259, ISS 5, 1998, P457-67 ISSN: 0026-8925 Coden: NGP
Language: ENGLISH
Document Type: JOURNAL ARTICLE

Specific mgi mutations in the alpha, beta or gamma subunits of the mitochondrial F1-ATPase have previously been found to suppress rho0 lethality in the petite-negative *yeast"** Kluyveromyces lactis. To *determine"** whether the suppressive activity of the altered F1 is dependent on the F0 sector of ATP synthase, we isolated and disrupted the genes KlATP4, 5 and 7, the three nuclear genes encoding subunits b, OSCP and d. Strains disrupted for any one, or all three of these genes are respiration deficient and have reduced viability. However a strain devoid of the three nuclear genes is still unable to lose mitochondrial DNA, whereas a mgi mutant with the three genes inactivated remains petite-positive. In the latter case, rho0 mutants can be isolated, upon treatment with ethidium bromide, that lack six major F0 subunits, namely the nucleus-encoded subunits b, OSCP and d, and the mitochondrially encoded Atp6, 8 and 9p. Production of rho0 mutants indicates that an F1-complex carrying a mgi mutation can assemble in the absence of F0 subunits and that suppression of rho0 lethality is an intrinsic property of the altered F1 particle.

12/3,AB/41 (Item 3 from file: 156)
DIALOG(R)File 156:Toxline(R)

03571850 Subfile: TOXBIB-98-303799

Aromatic hydrocarbon receptor polymorphism: development of new methods to correlate genotype with phenotype.

Maier A; Nebert DW

Center for Environmental Genetics and Department of Environmental Health, University of Cincinnati Medical Center, Cincinnati, OH 45267-0056, USA.

Source: Environ Health Perspect; VOL 106, ISS 7, 1998, P421-6 ISSN: 0091-6765 Coden: EI0

Language: ENGLISH

Document Type: JOURNAL ARTICLE

Differential CYP1A1 inducibility, reflecting variations in aromatic hydrocarbon receptor (AHR) affinity among inbred mouse strains, is an important determinant of environmental toxicity. We took advantage of the Ahr polymorphism in C57BL/6 and DBA/2 mice to develop an oligonucleotide-hybridization screening approach for the rapid identification of DNA sequence differences between Ahr alleles. Oligonucleotides containing single-base changes at polymorphic sites were immobilized on a solid support and hybridized with C57BL/6 or DBA/2 AHR cDNA radiolabeled probes. The observed hybridization patterns demonstrate that this approach can be used to detect nucleotide differences in the Ahr coding region with very high accuracy. In parallel experiments, we used a yeast two-hybrid system to assess phenotypic differences in AHR function. AHR activation, as measured by ss-galactosidase reporter activity in *Saccharomyces"** cerevisiae strain SFY526, was *determined"** following treatment with varying doses of the AHR ligand ss-naphthoflavone (BNF). We

found that the C57BL/6 AHR has about a 15-fold higher affinity for BNF than the DBA/2 AHR, in much better agreement with results reported for whole-animal studies than the values observed by in vitro ligand-binding assays. Using C57BL/6 and DBA/2 AHR chimeric proteins, we also confirmed the previously reported observation that an A375V change is principally responsible for the high- to low-affinity AHR phenotype. There has been no straightforward method to reliably and reproducibly phenotype large numbers of humans for CYP1A1 inducibility or AHR affinity. Screening human AHR cDNAs by oligonucleotide-hybridization and yeast two-hybrid methodologies will be invaluable for the rapid and unequivocal determination of changes in DNA sequence and receptor-ligand affinities associated with human AHR polymorphisms.

12/3,AB/42 (Item 1 from file: 35)
DIALOG(R)File 35:Dissertation Abstracts Online

01578698 AAD9733295
FUNCTIONAL ANALYSIS OF THE ROLES OF HOXD-13 AND HOXD-11 DURING CHICK LIMB DEVELOPMENT (BONE DEVELOPMENT, TRANSCRIPTION FACTORS)
Author: GOFF, DEBORAH JEANNE
Degree: PH.D.
Year: 1997
Corporate Source/Institution: HARVARD UNIVERSITY (0084)
Source: VOLUME 58/05-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 2271. 145 PAGES

Hox genes are important regulators of limb pattern in vertebrate development and display complex expression patterns. Misexpression of Hox genes in chicks using retroviral vectors provides an opportunity to analyze gain-of-function phenotypes and to assess their modes of action. In this thesis I report the misexpression phenotype for Hoxd-13 and compare it to the misexpression phenotype of Hoxd-11. Hoxd-13 misexpression in the hindlimb results in a shortening of the long bones, including the femur, the tibia, the fibula, and the tarsometatarsals. The changes in bone lengths caused by Hoxd-13 misexpression are late phenotypes that first become apparent during the growth phase of the bones. Analysis of tritiated thymidine uptake by the tibia and fibula demonstrates that Hox genes can pattern the limb skeleton by regulating the rates of cell division in the proliferative zone of growing cartilage. Hoxd-11, in contrast to Hoxd-13, acts both at the initial cartilage condensation phase in the foot and during the later growth phase in the lower leg.

Hox proteins are transcription factors which are hypothesized to control the expression of target genes during development. In a separate set of experiments, a yeast two-hybrid system was used to isolate proteins expressed during limb development which interact with Hoxd-11. Nine clones were selected which interact with a Hoxd-11/lexA bait, and DNA sequence

analysis indicates that some of these genes are homologous to known nuclear factors, among them PIC1, KAP1, UBC9, and the p18 subunit of the transcription factor SIII. The expression of some of these clones was analyzed by whole mount in *situ"** *hybridization"** in chick embryos. The PIC1 homolog was found to be expressed throughout both the forelimbs and hindlimbs, in the tectum, and in a posterior-to-anterior gradient from the tail into the mid-trunk region. The UBC9 homolog was found to be expressed similarly to the PIC1 homolog in the limbs and tectum, but is equally intense from the tail to the head. Further experiments are required to *determine"** if these interactions *detected"** in *yeast"** are physiologically relevant.

12/3,AB/43 (Item 2 from file: 35)
DIALOG(R)File 35:Dissertation Abstracts Online

01530572 AAD9705510
CHARACTERIZATION OF THE ARABIDOPSIS FLORAL HOMEOTIC GENE APETALA1
Author: GUSTAFSON-BROWN, CYNTHIA
Degree: PH.D.
Year: 1996
Corporate Source/Institution: UNIVERSITY OF CALIFORNIA, SAN DIEGO (0033)
Source: VOLUME 57/09-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 5459. 109 PAGES

The Arabidopsis floral homeotic gene APETALA1 (AP1) encodes a putative transcription factor that acts locally to specify the identity of the floral meristem, and to determine sepal and petal development. RNA in *situ"** *hybridization"** studies show that AP1 RNA accumulates uniformly throughout young floral primordia, but is absent from the inflorescence meristem. Later in development, AP1 RNA is excluded from cells that will give rise to the two inner whorls of organs. Here I show that the organ identity gene AGAMOUS prevents AP1 RNA accumulation in the two inner whorls of wild-type flowers. These and other data presented here lead to a revised model for the regulatory interactions among the genes specifying floral organ identity in Arabidopsis.

Also included is a detailed study of the regulation of Ap1 in floral and inflorescence meristems by LEAFY (LFY) and TERMINAL FLOWER (TFL). TFL represses AP1 RNA accumulation in inflorescence meristems. In plants synchronized to flower, AP1 and LFY are expressed in floral meristems by 48 hours after floral induction. Our data in lfy single mutants and in tfl lfy ap1 triple mutants, together with previous genetic data, suggest that initially AP1 activation is LFY-dependent, but that it later becomes LFY-independent. The factors involved in the LFY-independent activation of AP1 have yet to be *determined"**.

I utilized the *yeast"** two-hybrid system as a method to investigate the potential direct interactions of the floral meristem-identity genes,

AP1, LFY, CAULIFLOWER (CAL), and APETALA2. The four putative transcription factors are expressed in overlapping domains and have partially redundant functions. I found that AP1 forms homodimers in yeast, but CAL homodimers and AP1/CAL heterodimers were not detected. Other associations were less definitive. I then proceeded to search for additional proteins which interact with AP1 and CAL. From an Arabidopsis expression library generated from whole plant tissue, I identified four floral-specific MADS-domain proteins on the basis of their ability to interact with CAL. AP1 is also able to form heterodimers with these proteins, encoded by previously identified AGAMOUS-like genes.

12/3,AB/44 (Item 3 from file: 35)
DIALOG(R)File 35:Dissertation Abstracts Online

01262053 AAD9304089
STUDIES ON THE STRUCTURAL ORGANIZATION OF THE YEAST NUCLEUS USING EM IN *SITU"** *HYBRIDIZATION"** (EM *HYBRIDIZATION"**, SACCHAROMYCES CEREVISIAE, CRYOSECTIONING)
Author: DVORKIN, NADJA
Degree: PH.D.
Year: 1992
Corporate Source/Institution: UNIVERSITY OF CALIFORNIA, IRVINE (0030)
Source: VOLUME 53/09-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 4500. 133 PAGES

The development and application of an in *situ"** *hybridization"** technique combining non-isotopically labeled probes to isolated *yeast"** nuclei with electron microscopic immunogold *detection"** is described. Questions regarding the location of rDNA, precursor rRNA and small nuclear RNAs involved in rRNA and mRNA processing in nuclei and the relationships among these sequences in wildtype and mutant Saccharomyces cerevisiae are addressed.

In addition, the location of centromere and telomere sequences in Schizosaccharomyces pombe is investigated demonstrating the applicability of electron microscopic in *situ"** *hybridization"** to a variety of questions in these well-characterized model systems. Finally, the development of cryoprotection and cryosectioning techniques in yeast systems is presented.

12/3,AB/45 (Item 4 from file: 35)
DIALOG(R)File 35:Dissertation Abstracts Online

1040580 AAD8902807
MOLECULAR CLONING AND EXPRESSION OF THE ALPHA AND BETA TUBULIN GENES OF

MUCOR RACEMOSUS

Author: MEDINA, JOHN JAMES

Degree: PH.D.
Year: 1988
Corporate Source/Institution: WASHINGTON STATE UNIVERSITY (0251)
Source: VOLUME 49/11-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 4694. 115 PAGES

The role of the alpha and beta tubulin proteins and genes was examined in the morphogenesis of the dimorphic zygomycete Mucor racemosus. The gradual increase of a 55,000 dalton anti-tubulin immune reactive protein was observed during a yeast-to-hyphal morphological shift of this fungus. It was determined that this protein signal was specific to the hyphal morphological form and was composed of a number of separate protein moieties. These tubulin-specific antigens appeared in a coordinated fashion at different intervals throughout the length of the shift. Further analysis demonstrated that several of these antigens possessed alpha tubulin specific epitopes.

One alpha and three beta tubulin genes were isolated from an EMBL4 lambda library of Mucor DNA. Southern analysis employing cDNA probes from chicken brain embryo revealed multiple gene copies hybridizing at high stringencies within the fungal genome. In *situ"** *hybridization"** utilizing the cDNA probes yielded 10 alpha tubulin isolates and 12 beta tubulin isolates from the genomic library of Mucor DNA. Subsequent restriction analysis of the alpha tubulin isolates revealed the presence of a single, common region of homology approximately 2.8 kb in length. Restriction analysis of the 12 beta tubulin isolates detected the presence of three separate regions of homology. None of these regions shared common sequences with each other outside of their homology to avian tubulin DNA. They were thus assigned to separate loci within the genome. Transcriptional analysis indicated the presence of a single 1.2 kb alpha tubulin band in Mucor hyphal polyadenylated mRNA. A single 1.2 kb alpha tubulin band similarly *detected"** in the *yeast"** form of Mucor. Two beta tubulin mRNA sequences of 1.3 and 1.1 kb in size were also detected in the hyphal form.

12/3,AB/46 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04255643 H.W. WILSON RECORD NUMBER: BGSA00005643
Meiotic chromosomes: integrating structure and function.
AUGMENTED TITLE: review
Zickler, D
Kleckner, N
Annual Review of Genetics v. 33 (1999) p. 603-754
SPECIAL FEATURES: bibl il ISSN: 0066-4197

LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 73948

ABSTRACT: Meiotic chromosomes have been studied for many years, in part because of the fundamental life processes they represent, but also because meiosis involves the formation of homolog pairs, a feature which greatly facilitates the study of chromosome behavior. The complex events involved in homolog juxtaposition necessitate prolongation of prophase, thus permitting resolution of events that are temporally compressed in the mitotic cycle. Furthermore, once homologs are paired, the chromosomes are connected by a specific structure: the synaptonemal complex. Finally, interaction of homologs includes recombination at the DNA level, which is intimately linked to structural features of the chromosomes. In consequence, recombination-related events report on diverse aspects of chromosome morphogenesis, notably relationships between sisters, development of axial structure, and variations in chromatin status. The current article reviews recent information on these topics in an historical context. This juxtaposition has suggested new relationships between structure and function. Additional issues were addressed in a previous chapter (551). Reprinted by permission of the publisher.

12/3,AB/47 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04255640 H.W. WILSON RECORD NUMBER: BGSA00005640
Plant retrotransposons.
AUGMENTED TITLE: review
Kumar, Amar
Bennetzen, Jeffrey L
Annual Review of Genetics v. 33 (1999) p. 479-532
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 22407

ABSTRACT: Retrotransposons are mobile genetic elements that transpose through reverse transcription of an RNA intermediate. Retrotransposons are ubiquitous in plants and play a major role in plant gene and genome evolution. In many cases, retrotransposons comprise over 50% of nuclear DNA content, a situation that can arise in just a few million years. Plant retrotransposons are structurally and functionally similar to the retrotransposons and retroviruses that are found in other eukaryotic organisms. However, there are important differences in the genomic organization of retrotransposons in plants compared to some other eukaryotes, including their often-high copy numbers, their extensively

heterogeneous populations, and their chromosomal dispersion patterns. Recent studies are providing valuable insights into the mechanisms involved in regulating the expression and transposition of retrotransposons. This review describes the structure, genomic organization, expression, regulation, and evolution of retrotransposons, and discusses both their contributions to plant genome evolution and their use as genetic tools in plant biology. Reprinted by permission of the publisher.

12/3,AB/48 (Item 3 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04014417 H.W. WILSON RECORD NUMBER: BGSI99014417
Sodium-coupled transporters for Krebs cycle intermediates.
AUGMENTED TITLE: review
Pajor, Ana M
Annual Review of Physiology (Annu Rev Physiol) v. 61 ('99) p. 663-82
SPECIAL FEATURES: bibl il ISSN: 0066-4278
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 9112

ABSTRACT: Krebs ce life cycle.

12/3,AB/55 (Item 1 from file: 151)
DIALOG(R)File 151:HealthSTAR

03529510 20017711
Mapping studies on a pericentric inversion (18) (p11.31 q21.1) in a family with both schizophrenia and learning disability.
Hampson RM; Malloy MP; Mors O; Ewald H; Flannery AV; Morten J; Porteous DJ; Muir WJ; Blackwood DH
Department of Psychiatry, Edinburgh University, UK. Markh@hgu.mrc.ac.uk
Psychiatr Genet (ENGLAND) Sep 1999, 9 (3) p161-3,
ISSN: 0955-8829 JOURNAL CODE: B3X
Languages: ENGLISH
Document Type: JOURNAL ARTICLE
Chromosomal abnormalities that co-occur with psychiatric disorders can be useful direct pointers to the locus of susceptibility genes. Two families with pericentric inversions of chromosome 18, inv 18(p11.3 q21.1) and psychiatric illness have previously been described. We have fine mapped the chromosomal breakpoints of the rearrangement in a clinically well, inversion carrier from one of these families where other inversion carriers suffered from chronic schizophrenia or severe learning disability. Yeast artificial chromosomes (YACs) from the Whitehead/MIT physical maps of human

chromosome 18 have been positioned relative to the chromosomal breakpoints and a number of YACs that span these breakpoints have been identified. Linkage and association studies have previously suggested these regions of chromosome 18q and 18p as candidate loci harbouring genes involved in bipolar disorder and schizophrenia.

12/3,AB/56 (Item 1 from file: 442)
DIALOG(R)File 442:AMA Journals

00087889

Clinical Diagnostic Applications of the Polymerase Chain Reaction Infection and Rejection (ARTICLE)

RETTINGER, STEVEN D.; HAFENRICHTER, DANIEL G.; FLYE, M. WAYNE
Archives of Surgery
Nov, 1993; Original Article: p1253
LINE COUNT: 00744

In this review, we describe the power and sensitivity of the polymerase chain reaction and indicate areas of clinical medicine in which it is currently being applied. As this technology and automation improves and is simplified, its realm of application will expand, but its major impact will continue to be its facilitation of early, specific diagnoses in infectious disease, genetics, cancer, and transplantation. Polymerase chain reaction is currently most useful in the care of opportunistic infections in immunosuppressed hosts and in making the distinction between infection and rejection in transplant recipients. As the technique becomes more widely available and less costly, its application should minimize the need for broad-spectrum antibiotic therapy of infections, lower costs, andperhaps even shorten hospitalization. These potential beneficial effects of polymerase chain reaction will be particularly relevant inthe current cost-conscious health-care environment. (Arch Surg. 1993;128:1253-1259)

12/3,AB/57 (Item 2 from file: 442)
DIALOG(R)File 442:AMA Journals

00050902

The Role of the Clinical Microbiology Laboratory in Transplantation (Article)

Walker, Randall C., MD

Archives of Pathology & Laboratory Medicine
1991; 115: 299 (7)

The clinical microbiology laboratory plays a central role in any transplantation program. Pretransplantation microbiologic testic often determines prophylactic treatment, donor selection, and blood product use. With suspected infection, rapid microbiologic tests permit prompt therapy but are challenged by an ever-changing diversity of potential pathogens and limited specimen size. Antigen detection and the polymerase chain reaction with nucleic acid hybridization are newer methods that promise earlier detection of such serious infections as disseminated aspergillosis and primary cytomegalovirus and may reveal new microbial causes of various post-transplantation syndromes.

12/3,AB/58 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0264611 DBA Accession No.: 2001-04365 PATENT
Probe and probe sets suitable for detecting, identifying or quantifying the presence of Dekkera/Brettanomyces yeast, particularly Dekkera bruxellensis (Brettanomyces) in wineries and breweries - enzyme-linked DNA probe and fluorescent label for DNA detection
AUTHOR: Hyldig-Nielsen J J; O'Keefe H P; Stender H
CORPORATE SOURCE: Bedford, MA, USA.
PATENT ASSIGNEE: Boston-Probes 2000
PATENT NUMBER: WO 200077259 PATENT DATE: 20001221 WPI ACCESSION NO.: 2001-071284 (2008)
PRIORITY APPLIC. NO.: US 139212 APPLIC. DATE: 19990615
NATIONAL APPLIC. NO.: WO 2000US16273 APPLIC. DATE: 20000614
LANGUAGE: English
ABSTRACT: A DNA probe (P1) and DNA probe sets (S1) suitable for detecting, identifying or quantifying the presence of Dekkera sp. or Brettanomyces sp., particularly Dekkera bruxellensis (Brettanomyces) in a sample of interest, are claimed. Also claimed are: an enzyme-linked DNA probe suitable for use in an in *situ"** *hybridization"** assay and further characterized in that it has a probing nucleobase sequence directed to a *yeast"** specific target sequence; *detecting"**, identifying or quantifying *yeast"** in a sample of interest by: contacting 1 or more species of yeast in the sample with 1 or more yeast specific enzyme-linked DNA probes, under suitable in *situ"** *hybridization"** conditions, to form 1 or more DNA probe/target sequence hybrids within the *yeast"**; and *detecting"** enzyme-activity within the *yeast"** to *determine"** the presence, absence or number of *yeast"** sought to be *detected"** in the sample; a kit suitable for performing an assay that *detects"** or identifies *Dekkera"** sp. or *Brettanomyces"** sp.; and quantitating slow growing yeast in a liquid

sample in less than 48 hr. P1 and S1 are useful for *detection"** of *yeast"** in food, pharmaceutical products, clinical samples or environmental samples. (51pp)

12/3,AB/59 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0264014 DBA Accession No.: 2001-03768 PATENT
Assay for detecting microorganisms, especially Salmonella, comprises in *situ"** *hybridization"** of detectable nucleic acid probes followed by release and detection of hybridized probes - using DNA probe
AUTHOR: Snaidr J
CORPORATE SOURCE: Munich, Germany.
PATENT ASSIGNEE: Vermiccon-Engineering-Microbiology 2000
PATENT NUMBER: DE 19936875 PATENT DATE: 20001116 WPI ACCESSION NO.: 2001-026090 (2004)
PRIORITY APPLIC. NO.: DE 1036875 APPLIC. DATE: 19990805
NATIONAL APPLIC. NO.: DE 1036875 APPLIC. DATE: 19990805
LANGUAGE: German
ABSTRACT: An assay for detecting microorganisms in a sample by fixing the microorganisms, incubating the microorganisms with detectable DNA probe, removing unhybridized DNA probes, releasing hybridized DNA probes and detecting and optionally quantitating the released DNA probe molecules, is new. Also claimed is a kit for performing the assay, containing at least one hybridization buffer and at least one DNA probe for specifically detecting a microorganism and at least one DNA probe for performing a negative control. The assay is useful for *detecting"** and optionally quantitating *yeasts"**, bacteria, algae or fungi, especially Salmonella sp. bacteria, in environmental samples, wastewater treatment samples, films and pharmaceutical or cosmetic products. (18pp)

12/3,AB/60 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0128752 DBA Accession No.: 92-01244
*Detection"** and characterization of chimeric *yeast"** artificial chromosome clones - for the isolation of single, large chromosomal DNA segments
AUTHOR: Green E D; Riethman H C; Dutchik J E; Olson M V
CORPORATE SOURCE: Department of Genetics, Washington University School of Medicine, St. Louis, Missouri 63110, USA.
JOURNAL: Genomics (11, 3, 658-69) 1991
CODEN: GNMCEP

LANGUAGE: English
ABSTRACT: Methods for the construction of yeast artificial chromosome (YAC) clones were designed in order to isolate single, large (100-1000 kb) segments of chromosomal DNA. The major artifact in YAC clones is the formation of YACs containing 2 or more unrelated pieces of DNA. Methods for detecting such chimerical YACs clones were investigated. The primary characterization involved the development of sequence-tagged sites (STSs) from the ends of the inserts and the assignment of these STSs to particular human chromosomes by PCR analysis of DNA from a panel of human-hamster hybrid cell lines. Confirmatory data were also acquired using phage lambda subclones containing the ends of the YAC inserts as probes in fluorescent in *situ"** *hybridization"** assays of human metaphase chromosomes. The detailed characterization of a chimeric YAC, yCF-1, isolated from a library prepared from total human DNA was described. The organization of this clone indicated that it formed by in vivo recombination, presumably in Saccharomyces cerevisiae, between 2 Alu sequences located on unrelated segments of human DNA. (46 ref)

12/3,AB/61 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0110671 DBA Accession No.: 90-13362
Investigation of yeast plasmid maintenance using techniques for the analysis of individual cells - plasmid copy number *determination"** in *Saccharomyces"** cerevisiae (conference abstract)
AUTHOR: Albury M S; Wheals A E; Cashmore A M
CORPORATE SOURCE: Department of Genetics, University of Leicester, Leicester LE1 7RH, UK.
JOURNAL: Yeast (6, Spec. Issue,) 1990
CODEN: YESTE3
LANGUAGE: English
ABSTRACT: An in *situ"** *hybridization"** method was developed for the direct measurement of plasmid copy number in single Saccharomyces cerevisiae cells. 32P labeled probes to regions of the native plasmid were used to obtain specific hybridization. Isogenic plasmid-containing and plasmid-free cells were used as controls. In order to quantitate the method and to determine the sensitivity of detection, a series of control strains was constructed with part of the plasmid 2-um stably integrated into the chromosome. The use of 2-um probes for hybridization to these integrated strains with probes hybridizing to ribosomal DNA allowed the measurement of the distribution of hybridization signal due to experimental variation. Non-radioactive detection methods involving the use of non-isotopically labeled DNA probes and immunofluorescence techniques were developed for the use of fluorimetry to analyze large numbers of individual cells for the

accurate determination of the distribution of plasmid molecules. (0 ref)

12/3,AB/62 (Item 1 from file: 370)
DIALOG(R)File 370:Science

00510324
A Phospholipase C-Dependent Inositol Polyphosphate Kinase Pathway Required for Efficient Messenger RNA Export
York, John D.<CRF RID="C1"> ; Odom, Audrey R.; Murphy, Robert; Ives, Eric B.; Wente, Susan R.<CRF RID="C1">
Departments of Pharmacology and Cancer Biology and of Biochemistry, Duke University Medical Center, DUMC 3813, Durham, NC 27710, USA. Department of Cell Biology and Physiology, Box 8228, Washington University School of Medicine, 660 South Euclid, St. Louis, MO 63110, USA.
Science Vol. 285 5424 pp. 96
Publication Date: 7-02-1999 (990702) Publication Year: 1999
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: REPORTS
Word Count: 2482

Abstract: In order to identify additional factors required for nuclear export of messenger RNA, a genetic screen was conducted with a yeast mutant deficient in a factor Gle1p, which associates with the nuclear pore complex (NPC). The three genes identified encode phospholipase C and two potential inositol polyphosphate kinases. Together, these constitute a signaling pathway from phosphatidylinositol 4,5-bisphosphate to inositol hexakisphosphate (IP.inf(6)). The common downstream effects of mutations in each component were deficiencies in IP.inf(6) synthesis and messenger RNA export, indicating a role for IP.inf(6) in GLE1 function and messenger RNA export.

12/3,AB/63 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

013587077
WPI Acc No: 2001-071284/200108
XRAM Acc No: C01-019986
Probe and probe sets suitable for detecting, identifying or quantifying the presence of Dekkera/Brettanomyces yeast, particularly Dekkera bruxellensis (Brettanomyces) in wineries and breweries
Patent Assignee: BOSTON PROBES INC (BOST-N)

Inventor: HYLDIG-NIELSEN J J; O'KEEFE H P; STENDER H
Number of Countries: 019 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200077259	A1	20001221	WO 2000US16273	A	20000614	200108	B

Priority Applications (No Type Date): US 99139212 A 19990615
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200077259	A1	E	51	C12Q-001/68	

Designated States (National): JP
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
Abstract (Basic): WO 200077259 A1
Abstract (Basic):

NOVELTY - Probe (P1) and probe sets (S1) suitable for detecting, identifying or quantitating the presence of Dekkera/Brettanomyces yeast, particularly Dekkera bruxellensis (Brettanomyces) in a sample of interest, are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an enzyme-linked probe (P2) suitable for use in an in-*situ"** *hybridization"** assay and further characterized in that it comprises a probing nucleobase sequence directed to a yeast specific target sequence;

(2) a method (M1) for *detecting"**, identifying or enumerating *yeast"** in a sample of interest, comprising:

(a) contacting one or more species of yeast in the sample with one or more yeast specific enzyme-linked probes, under suitable in-*situ"** *hybridization"** conditions, to form one or more probe/target sequence hybrids within the yeast; and

(b) *detecting"** enzyme activity within the *yeast"** to *determine"** the presence, absence or number of *yeast"** sought to be *detected"** in the sample;

(3) a kit suitable for performing an assay that *detects"**, identifies or *Dekkera"**/*Brettanomyces"** *yeast"** in a sample, comprising:

(a) one or more Dekkera/Brettanomyces specific probes; and

(b) other reagents or compositions necessary to perform the assay; and

(4) a method for quantitating slow growing yeast in a liquid sample in less than 48 hours, comprising:

(a) filtering a fixed volume of liquid using a filter having a pore size that does not allow the yeast to pass;

(b) incubating the filter containing the yeast, in a suitable medium for 45 hours or less;

(c) fixing the microcolonies of yeast to the filter;

(d) contacting the microcolonies of yeast with a yeast specific

enzyme-linked probe to form one or more probe/target sequence hybrids within the yeast;

(e) *detecting"** enzyme activity within the *yeast"** to *determine"** the presence, absence or number of *yeast"** sought to be *detected"** in the sample; and

(f) *determining"** the quantity of *yeast"** in the sample.

USE - The probes and probe sets are useful for the *detection"** of *Dekkera"**/*Brettanomyces"** *yeast"** in particularly Dekkera bruxellensis (Brettanomyces) in wineries and breweries. The probes and probe sets are also useful for *detection"** of *yeast"** in food, pharmaceutical products, personal care products, dairy products, environmental samples, clinical samples and/or beverages.

pp; 51 DwgNo 0/2

12/3,AB/64 (Item 2 from file: 351)
DIALOG(R)File 351:Derwent WPI

013541884
WPI Acc No: 2001-026090/200104
XRAM Acc No: C01-008206

Assay for detecting microorganisms, especially Salmonella, comprises in *situ"** *hybridization"** of detectable nucleic acid probes followed by release and detection of hybridized probes

Patent Assignee: VERMICON AG (VERM-N); VERMICON ENG & MICROBIOLOGY AG (VERM-N)
Inventor: SNAIDR J
Number of Countries: 090 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
DE 19936875	A1	20001116	DE 1036875	A	19990805	200104	B
WO 200068421	A2	20001116	WO 2000EP3989	A	20000504	200104	
AU 200049163	A	20001121	AU 200049163	A	20000504	200112	

Priority Applications (No Type Date): DE 1021281 A 19990507
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
DE 19936875	A1		18	C12Q-001/68	
WO 200068421	A2	G		C12Q-001/68	

Designated States (National): AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW

AU 200049163	A		C12Q-001/68	Based on patent WO 200068421

Abstract (Basic): DE 19936875 A1
Abstract (Basic):

NOVELTY - Assay for detecting microorganisms in a sample, comprising fixing the microorganisms, incubating the microorganisms with detectable nucleic acid probe molecules, removing unhybridized probe molecules, releasing hybridized probe molecules, and detecting and optionally quantitating the released probe molecules.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a kit for performing the assay, comprising at least one hybridization buffer and at least one nucleic acid probe for specifically detecting a microorganism and at least one nucleic acid probe for performing a negative control.

USE - The assay is useful for *detecting"** and optionally quantitating *yeasts"**, bacteria, algae or fungi, especially Salmonella bacteria, in environmental samples (especially water, soil and air), foodstuffs (especially milk, dairy products, drinking water, beverages, bakery products and meat), wastewater treatment samples (especially activated sludge or anaerobic sludge), biofilms and pharmaceutical or cosmetic products.

ADVANTAGE - The assay can be performed using inexpensive equipment, e.g. a fluorimeter rather than an epifluorescence microscope.

pp; 18 DwgNo 0/2

12/3,AB/65 (Item 1 from file: 444)
DIALOG(R)File 444:New England Journal of Med.

00120972

Genomic Aberrations and Survival in Chronic Lymphocytic Leukemia (Original Articles)

Dohner, Hartmut; Stilgenbauer, Stephan; Benner, Axel; Leupolt, Elke; Krober, Alexander; Bullinger, Lars; Dohner, Konstanze; Bentz, Martin; Lichter, Peter.
The New England Journal of Medicine
Dec 28, 2000; 343 (26),pp 1910-1916
LINE COUNT: 00269 WORD COUNT: 03725

Abstract

Background: Fluorescence in *situ"** *hybridization"** has improved the detection of genomic aberrations in chronic lymphocytic leukemia. We used this method to identify chromosomal abnormalities in patients with chronic lymphocytic leukemia and assessed their prognostic implications.

Methods: Mononuclear cells from the blood of 325 patients with chronic lymphocytic leukemia were analyzed by fluorescence in *situ"**

*hybridization"** for deletions in chromosome bands 6q21, 11q22-23, 13q14, and 17p13; trisomy of bands 3q26, 8q24, and 12q13; and translocations involving band 14q32. Molecular cytogenetic data were correlated with clinical findings.

Results: Chromosomal aberrations were detected in 268 of 325 cases (82 percent). The most frequent changes were a deletion in 13q (55 percent), a deletion in 11q (18 percent), trisomy of 12q (16 percent), a deletion in 17p (7 percent), and a deletion in 6q (6 percent). Five categories were defined with a statistical model: 17p deletion, 11q deletion, 12q trisomy, normal karyotype, and 13q deletion as the sole abnormality; the median survival times for patients in these groups were 32, 79, 114, 111, and 133 months, respectively. Patients in the 17p- and 11q-deletion groups had more advanced disease than those in the other three groups. Patients with 17p deletions had the shortest median treatment-free interval (9 months), and those with 13q deletions had the longest (92 months). In multivariate analysis, the presence or absence of a 17p deletion, the presence or absence of an 11q deletion, age, Binet stage, the serum lactate dehydrogenase level, and the white-cell count gave significant prognostic information.

Conclusions: Genomic aberrations in chronic lymphocytic leukemia are important independent predictors of disease progression and survival. These findings have implications for the design of risk-adapted treatment strategies. (N Engl J Med 2000;343:1910-6.)

12/3,AB/66 (Item 1 from file: 65)
DIALOG(R)File 65:Inside Conferences

00949131 INSIDE CONFERENCE ITEM ID: CN009264607
Sites of nuclear localization of a reporter transcript in *yeast"** *determined"** by fluorescence in *situ"** *hybridization"**
Long, R. M.; Elliott, D. J.; Rosbash, M.; Singer, R. H.
CONFERENCE: RNA processing-Meeting
ABSTRACTS OF PAPERS PRESENTED AT THE MEETING ON RNA PROCESSING , 1995
P: 128
Cold Spring Harbor Laboratory, 1995
LANGUAGE: English DOCUMENT TYPE: Conference Abstracts and programme
CONFERENCE SPONSOR: Cold Spring Harbor Laboratory
CONFERENCE LOCATION: Cold Spring Harbor, NY
CONFERENCE DATE: May 1995 (199505) (199505)

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        03may01 13:30:53 User219783 Session D1704.2

SYSTEM:OS  - DIALOG OneSearch
  File 144:Pascal  1973-2001/Apr W5
         (c) 2001 INIST/CNRS
  File 266:FEDRIP  2001/Apr
         Comp & dist by NTIS, Intl Copyright All Rights Res
  File  50:CAB Abstracts  1972-2001/Mar
         (c) 2001 CAB International
*File  50: Truncating CC codes is recommended for full retrieval.
See Help News50 for details.
  File 149:TGG Health&Wellness DB(SM)  1976-2001/Apr W4
         (c) 2001 The Gale Group
  File 484:Periodical Abstracts Plustext  1986-2001/Apr W5
         (c) 2001 Bell & Howell
  File 399:CA SEARCH(R)  1967-2001/UD=13419
         (c) 2001 AMERICAN CHEMICAL SOCIETY
*File 399: Use is subject to the terms of your user/customer agreement.
RANK charge added; see HELP RATES 399.
  File  10:AGRICOLA  70-2001/Apr
         (c) format only 2001 The Dialog Corporation
  File 156:Toxline(R)  1965-2000/Dec
         (c) format only 2000 The Dialog Corporation
*File 156: Final updates for this file have been loaded and this
file is now closed. For changes to the file please see Help News156.
  File  35:Dissertation Abstracts Online  1861-2001/May
         (c) 2001 UMI
  File  98:General Sci Abs/Full-Text  1984-2001/Mar
         (c) 2001 The HW Wilson Co.
  File 151:HealthSTAR  1975-2000/Dec
         (c) format only 2000 The Dialog Corporation
*File 151: Final updates for this file have been loaded and the
file is now closed. Please see Help News151 for changes to the file.
  File 442:AMA  Journals  1982-2001/Apr B3
         (c)2001 Amer Med Assn -FARS/DARS apply
*File 442: There is no data missing. UDs have been adjusted to reflect
the current months data. See Help News442 for details.
  File 357:Derwent Biotechnology Abs  1982-2001/May B1
         (c) 2001 Derwent Publ Ltd
*File 357: Price changes as of 1/1/01. Please see HELP RATES 357.
  File 370:Science  1996-1999/Jul W3
         (c) 1999 AAAS
  File 351:Derwent WPI  1963-2001/UD,UM &UP=200123
         (c) 2001 Derwent Info Ltd
*File 351: Price changes as of 1/1/01. Please see HELP RATES 351.
 72 Updates in 2001. Please see HELP NEWS 351 for details.
  File  94:JICST-EPlus  1985-2001/Apr W2
         (c)2001 Japan Science and Tech Corp(JST)
```

Searcher : Shears 308-4994

*File 94: There is no data missing. UDs have been adjusted to reflect the current months data. See Help News94 for details.
File 444:New England Journal of Med. 1985-2001/May W1
(c) 2001 Mass. Med. Soc.
File 162:CAB HEALTH 1983-2001/Mar
(c) 2001 CAB INTERNATIONAL
*File 162: Truncating CC codes is recommended for full retrieval. See Help News162 for details.
File 172:EMBASE Alert 2001/Apr W4
(c) 2001 Elsevier Science B.V.
File 457:The Lancet 1986-2000/Oct W1
(c) 2000 The Lancet, Ltd.
*File 457: Due to production changes at The Lancet, the updating of this file is delayed.
File 16:Gale Group PROMT(R) 1990-2001/May 02
(c) 2001 The Gale Group
File 143:Biol. & Agric. Index 1983-2001/Mar
(c) 2001 The HW Wilson Co
File 203:AGRIS 1974-2001/Oct
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File 315:ChemEng & Biotec Abs 1970-2001/Jan
(c) 2001 DECHEMA
File 358:Current BioTech Abs 1983-2001/Jan
(c) 2001 DECHEMA
*File 358: Updates delayed. Please see HELP NEWS 358 for details.
File 77:Conference Papers Index 1973-2001/May
(c) 2001 Cambridge Sci Abs
File 65:Inside Conferences 1993-2001/Apr W5
(c) 2001 BLDSC all rts. reserv.
*File 65: CD=2000 and CY=2000 are not fully functioning. Please see Help News65 for details.
File 43:Health News Daily 1990-2001/Apr 20
(c) 2001 F-D-C reports Inc.
File 99:Wilson Appl. Sci & Tech Abs 1983-2001/Mar
(c) 2001 The HW Wilson Co.

Set	Items	Description
S2	505094	YEAST? ? OR DEKKERA OR BRETTANOMYC? OR CANDIDA OR SACCHAROMYC? OR CLAVISPOR?
S3	42	AU=("HYLDIG-NEILSEN, J"? OR "HYLDIG-NIELSEN J"? OR "NEILSEN-HYLDIG, J"? OR "NEILSEN-HYLDIG J"?)
S4	1	AU=(HYLDIG NEILSEN, J? OR HYLDIG NIELSEN J? OR NEILSEN HYLDIG, J? OR NEILSEN HYLDIG J?)
S5	57	AU=(HYLDIG, J? OR HYLDIG J? OR NEILSEN J? OR NEILSEN, J?)
S6	100	S3 OR S4 OR S5

- Author (s)

Searcher : Shears 308-4994

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S7          16   AU=(OKEEFE, H? OR OKEEFE H? OR "O'KEEFE, H"? OR "O'KEEFE H-
               "? OR O KEEFE, H? OR O KEEFE H?)
S8         183   AU=(STENDER, H? OR STENDER H?)
S9           2   S6 AND S7 AND S8
S10          7   S6 AND (S7 OR S8)
S11          3   S7 AND S8
S12          8   (S6 OR S7 OR S8) AND S2
S13         10   S9 OR S10 OR S11 OR S12
S14          9   RD (unique items)
>>>No matching display code(s) found in file(s): 43, 65

 14/3,AB/1      (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2001 INIST/CNRS. All rts. reserv.

  14977613   PASCAL No.: 01-0131065
  Identification of *Dekkera"** bruxellensis (*Brettanomyces"**) from wine
by fluorescence in situ hybridization using peptide nucleic acid probes
  *STENDER Henrik"**; KURTZMAN Cletus; *HYLDIG-NIELSEN Jens J"**; SOERENSEN
Ditte; BROOMER Adam; OLIVEIRA Kenneth; PERRY-O'KEEFE Heather; SAGE Andrew;
YOUNG Barbara; COULL James
  Boston Probes, Inc., Bedford, Massachusetts 01730, United States;
Microbial Properties Research Unit, National Center for Agricultural
Utilization Research, USDA Agricultural Research Service, Peoria, Illinois
61604, United States; Millipore Corporation, Bedford, Massachusetts 01730,
United States
  Journal: Applied and environmental microbiology : (Print),  2001, 67 (2)
938-941
  Language: English
  A new fluorescence in situ hybridization method using peptide nucleic
acid (PNA) probes for identification of *Brettanomyces"** is described. The
test is based on fluorescein-labeled PNA probes targeting a
species-specific sequence of the rRNA of *Dekkera"** bruxellensis. The PNA
probes were applied to smears of colonies, and results were interpreted by
fluorescence microscopy. The results obtained from testing 127 different
*yeast"** strains, including 78 *Brettanomyces"** isolates from wine, show
that the spoilage organism *Brettanomyces"** belongs to the species D.
bruxellensis and that the new method is able to identify *Brettanomyces"**
 (D. bruxellensis) with 100% sensitivity and 100% specificity.

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 14/3,AB/2      (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

  134052240    CA: 134(5)52240h    PATENT
```

Peptide nucleic acid probes targeting rRNA sequence and hybridization assay for wine spoiling Dekkera/Brettanomyces yeast detection
INVENTOR(AUTHOR): Hyldig-Nielsen, Jens J.; O'Keefe, Heather P.; Stender, Henrik
LOCATION: USA
ASSIGNEE: Boston Probes, Inc.
PATENT: PCT International ; WO 200077259 A1 DATE: 20001221
APPLICATION: WO 2000US16273 (20000614) *US PV139212 (19990615)
PAGES: 53 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A
DESIGNATED COUNTRIES: JP DESIGNATED REGIONAL: AT; BE; CH; CY; DE; DK; ES ; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE

14/3,AB/3 (Item 1 from file: 156)
DIALOG(R)File 156:Toxline(R)

03774114 Subfile: BIOSIS-00-05727
A probe-based method for rapid identification and enumeration of *Brettanomyces"** in wine.
*STENDER H"**; PERRY-O'KEEFE H; HYLDIG-NELSON JJ; BROOMER A; SARACINO M; KURTZMAN C; YOUNG B; COULL JM
Boston Probes, Inc., 75 E. Wiggins Ave., Bedford, MA, USA.
Source: ANNUAL MEETING OF THE AMERICAN SOCIETY FOR ENOLOGY AND VITICULTURE, RENO, NEVADA, USA, JUNE 30-JULY 2, 1999.YAMERICAN JOURNAL OF ENOLOGY AND VITICULTURE; 50 (3). 1999. 383-384. Coden: AJEVA
Language: ENGLISH
BIOSIS COPYRIGHT: BIOL ABS. RRM A PROBE-BASED METHOD FOR RAPID IDENTIFICATION AND ENUMERATION OF $*BRETTANOMYCES"** IN WINEYMEETING ABSTRACT *BRETTANOMYCES"** SPOILAGE *YEAST"** FOODS PROBE-BASED METHOD METHODOLOGY WINE SPOILAGE OFF-FLAVOR ENUMERATION METHOD IDENTIFICATION METHOD

14/3,AB/4 (Item 2 from file: 156)
DIALOG(R)File 156:Toxline(R)

03750964 Subfile: BIOSIS-00-01049
A new molecular method for simultaneous identification and enumeration of *Brettanomyces"** in wine.
*STENDER H"**; PERRY-O'KEEFE H; *HYLDIG-NIELSEN JJ"**; BROOMER A; SARACINO M; KURTZMAN C; YOUNG B; COULL JM
Boston Probes, Inc., Bedford, MA, USA.
Source: 99TH GENERAL MEETING OF THE AMERICAN SOCIETY FOR MICROBIOLOGY, CHICAGO, ILLINOIS, USA, MAY 30-JUNE 3, 1999.YABSTRACTS OF THE GENERAL MEETING OF THE AMERICAN SOCIETY FOR MICROBIOLOGY; 99 (0). 1999. 516.
Coden: AGMME

Language: ENGLISH
BIOSIS COPYRIGHT: BIOL ABS. RRMA NEW MOLECULAR METHOD FOR SIMULTANEOUS IDENTIFICATION AND ENUMERATION OF $*BRETTANOMYCES"** IN WINEYMEETING ABSTRACT MEETING POSTER *BRETTANOMYCES"** FOOD CONTAMINANT WINE FOODS METHODOLOGY 26S RRNA 26S RIBOSOMAL RNA IN SITU HYBRIDIZATION METHOD PEPTIDE NUCLEIC ACID PROBES ALCOHOLIC BEVERAGE FOOD CONTAMINANT DETECTION METHOD

14/3,AB/5 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0264611 DBA Accession No.: 2001-04365 PATENT
Probe and probe sets suitable for detecting, identifying or quantifying the presence of *Dekkera"**/*Brettanomyces"** *yeast"**, particularly *Dekkera"** bruxellensis (*Brettanomyces"**) in wineries and breweries - enzyme-linked DNA probe and fluorescent label for DNA detection
AUTHOR: *Hyldig-Nielsen J J"**; *O'Keefe H P"**; *Stender H"**
CORPORATE SOURCE: Bedford, MA, USA.
PATENT ASSIGNEE: Boston-Probes 2000
PATENT NUMBER: WO 200077259 PATENT DATE: 20001221 WPI ACCESSION NO.: 2001-071284 (2008)
PRIORITY APPLIC. NO.: US 139212 APPLIC. DATE: 19990615
NATIONAL APPLIC. NO.: WO 2000US16273 APPLIC. DATE: 20000614
LANGUAGE: English
ABSTRACT: A DNA probe (P1) and DNA probe sets (S1) suitable for detecting, identifying or quantifying the presence of *Dekkera"** sp. or *Brettanomyces"** sp., particularly *Dekkera"** bruxellensis (*Brettanomyces"**) in a sample of interest, are claimed. Also claimed are: an enzyme-linked DNA probe suitable for use in an in situ hybridization assay and further characterized in that it has a probing nucleobase sequence directed to a *yeast"** specific target sequence; detecting, identifying or quantifying *yeast"** in a sample of interest by: contacting 1 or more species of *yeast"** in the sample with 1 or more *yeast"** specific enzyme-linked DNA probes, under suitable in situ hybridization conditions, to form 1 or more DNA probe/target sequence hybrids within the *yeast"**; and detecting enzyme-activity within the *yeast"** to determine the presence, absence or number of *yeast"** sought to be detected in the sample; a kit suitable for performing an assay that detects or identifies *Dekkera"** sp. or *Brettanomyces"** sp.; and quantitating slow growing *yeast"** in a liquid sample in less than 48 hr. P1 and S1 are useful for detection of *yeast"** in food, pharmaceutical products, clinical samples or environmental samples. (51pp)

14/3,AB/6 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0248928 DBA Accession No.: 2000-03418 PATENT
Formation of peptide nucleic acid probe triplexes for detection, quantitation and analysis of nucleic acid target sequences - peptide nucleic acid probe triple helix
AUTHOR: Coull J; Stefano K; *Hyldig-Nielsen J J"**; *Stender H"**; Petersen K H
CORPORATE SOURCE: Bedford, MA, USA; Glostrup, Denmark.
PATENT ASSIGNEE: Boston-Probes 1999
PATENT NUMBER: WO 9955916 PATENT DATE: 19991104 WPI ACCESSION NO.: 2000-072188 (2006)
PRIORITY APPLIC. NO.: US 83649 APPLIC. DATE: 19980429
NATIONAL APPLIC. NO.: WO 99US9433 APPLIC. DATE: 19990429
LANGUAGE: English
ABSTRACT: A peptide nucleic acid probe (PNA probe) triple helix is formed by contacting a sample containing a target nucleic acid (T-NA) under hybridization conditions to at least one probe set comprising 3 probes where a 1st and 2nd probes comprise a probing segment and a PNA arm segment and where the 3rd probe comprises a PNA arm segment. Also claimed are: detecting or quantifying T-NA in a sample by detecting/quantifying the PNA probe triple helix, where the presence/amount of the triple helix indicates the presence/amount of T-NA in a sample; a set of 1st, 2nd and 3rd PNA probes; a probe/triple helix nucleic acid complex; and a kit for detecting/quantifying a T-NA in a sample. The methods, kits and probes are suited to improved detection, quantitation and analysis of T-NA using probe-based hybridization assays. The 3 component polymers and the T-NA interact to give a detectable signal, even in the presence of non-target sequences. The methods and probes improve the specificity and sensitivity of the assay, improving the signal to noise ratio. (83pp)

14/3,AB/7 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

013587077
WPI Acc No: 2001-071284/200108
XRAM Acc No: C01-019986
Probe and probe sets suitable for detecting, identifying or quantifying the presence of *Dekkera"**/*Brettanomyces"** *yeast"**, particularly *Dekkera"** bruxellensis (*Brettanomyces"**) in wineries and breweries
Patent Assignee: BOSTON PROBES INC (BOST-N)
Inventor: *HYLDIG-NIELSEN J J"**; *O'KEEFE H P"**; *STENDER H"**
Number of Countries: 019 Number of Patents: 001
Patent Family:
Patent No Kind Date Applicat No Kind Date Week

WO 200077259 A1 20001221 WO 2000US16273 A 20000614 200108 B

Priority Applications (No Type Date): US 99139212 A 19990615
Patent Details:
Patent No Kind Lan Pg Main IPC Filing Notes
WO 200077259 A1 E 51 C12Q-001/68
Designated States (National): JP
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
Abstract (Basic): WO 200077259 A1
Abstract (Basic):

NOVELTY - Probe (P1) and probe sets (S1) suitable for detecting, identifying or quantitating the presence of *Dekkera"**/*Brettanomyces"** *yeast"**, particularly *Dekkera"** bruxellensis (*Brettanomyces"**) in a sample of interest, are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an enzyme-linked probe (P2) suitable for use in an in-situ hybridization assay and further characterized in that it comprises a probing nucleobase sequence directed to a *yeast"** specific target sequence;

(2) a method (M1) for detecting, identifying or enumerating *yeast"** in a sample of interest, comprising:

(a) contacting one or more species of *yeast"** in the sample with one or more *yeast"** specific enzyme-linked probes, under suitable in-situ hybridization conditions, to form one or more probe/target sequence hybrids within the *yeast"**; and

(b) detecting enzyme activity within the *yeast"** to determine the presence, absence or number of *yeast"** sought to be detected in the sample;

(3) a kit suitable for performing an assay that detects, identifies or *Dekkera"**/*Brettanomyces"** *yeast"** in a sample, comprising:

(a) one or more *Dekkera"**/*Brettanomyces"** specific probes; and

(b) other reagents or compositions necessary to perform the assay; and

(4) a method for quantitating slow growing *yeast"** in a liquid sample in less than 48 hours, comprising:

(a) filtering a fixed volume of liquid using a filter having a pore size that does not allow the *yeast"** to pass;

(b) incubating the filter containing the *yeast"**, in a suitable medium for 45 hours or less;

(c) fixing the microcolonies of *yeast"** to the filter;

(d) contacting the microcolonies of *yeast"** with a *yeast"** specific enzyme-linked probe to form one or more probe/target sequence hybrids within the *yeast"**;

(e) detecting enzyme activity within the *yeast"** to determine the presence, absence or number of *yeast"** sought to be detected in the sample; and

(f) determining the quantity of *yeast"** in the sample.

USE - The probes and probe sets are useful for the detection of *Dekkera"**/*Brettanomyces"** *yeast"** in particularly *Dekkera"** bruxellensis (*Brettanomyces"**) in wineries and breweries. The probes and probe sets are also useful for detection of *yeast"** in food, pharmaceutical products, personal care products, dairy products, environmental samples, clinical samples and/or beverages.

pp; 51 DwgNo 0/2

14/3,AB/8 (Item 2 from file: 351)
DIALOG(R)File 351:Derwent WPI

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WPI Acc No: 2000-072188/200006
XRAM Acc No: C00-020557
Formation of peptide nucleic acid probe triplexes for detection, quantitation and analysis of nucleic acid target sequences
Patent Assignee: BOSTON PROBES INC (BOST-N); DAKO AS (DAKO-N)
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Number of Countries: 023 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 9955916	A1	19991104	WO 99US9433	A	19990429	200006	B
AU 9937750	A	19991116	AU 9937750	A	19990429	200015	
EP 1073767	A1	20010207	EP 99920194	A	19990429	200109	
			WO 99US9433	A	19990429		

Priority Applications (No Type Date): US 9883649 A 19980429; US 9870546 A 19980429
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 9955916	A1	E	83	C12Q-001/68	
Designated States (National): AU CA JP US					
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
AU 9937750	A			C12Q-001/68	Based on patent WO 9955916
EP 1073767	A1	E		C12Q-001/68	Based on patent WO 9955916
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					

Abstract (Basic): WO 9955916 A1
Abstract (Basic):

NOVELTY - A peptide nucleic acid (PNA) probe triplex is formed by contacting a sample containing a target nucleic acid under hybridization conditions to at least one probe set comprising three

probes where the first and second probes comprise a probing segment and a PNA arm segment and where the third probe comprises a PNA arm segment.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) a method for detecting the presence or quantity of target nucleic acid present in a sample, comprising detecting the presence or quantity of a PNA probe triplex, where the presence or quantity of the PNA probe triplex is indicative of the presence or quantity of target nucleic acid in the sample;

(2) a probe set comprising first, second and third probes as above;

(3) a probe triplex/target nucleic acid complex; and

(4) a kit suitable for detecting the presence or amount of target nucleic acid in a sample.

USE - The methods, kits and probes are suitable for the improved detection, quantitation and analysis of nucleic acid target sequences using probe-based hybridization assays.

ADVANTAGE - The three component polymers and the target nucleic acid interact in order to produce a detectable signal, even in the presence of non-target sequences. The methods, etc. improve the specificity and sensitivity of the assay thereby improving the signal to noise ratio of the assay. The PNA triplex structures exploit the advantages of using short probes as a means to achieve specificity while still possessing the sequence diversity associated with longer probes. Additionally, the PNA probe triplexes can be designed without regard to treatment considerations for the orientation of probes within the triplex.

pp; 83 DwgNo 0/11

14/3,AB/9 (Item 1 from file: 172)
DIALOG(R)File 172:EMBASE Alert

01969410 EMBASE No: 2001071334

Filter-based PNA in situ hybridization for rapid detection, identification and enumeration of specific micro-organisms

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LANGUAGES: ENGLISH SUMMARY LANGUAGES: ENGLISH

Aims: A method for rapid and simultaneous detection, identification and enumeration of specific micro-organisms using Peptide Nucleic Acid (PNA)

probes is presented. Methods and Results: The method is based on a membrane filtration technique. The membrane filter was incubated for a short period of time. The microcolonies were analysed by in situ hybridization, using peroxidase-labelled PNA probes targeting a species-specific rRNA sequence, and visualized by a chemiluminescent reaction. Microcolonies were observed as small spots of light on film, thereby providing simultaneous detection, identification and enumeration. The method showed 95-100% correlation to standard plate counts along with definitive identification due to the specificity of the probe. Conclusions: Using the same protocol, results were generated approximately three times faster than culture methods for Gram-positive and -negative bacterial species and *yeast"** species. Significance and Impact of the Study: The method is an improvement on the current membrane filtration technique, providing rapid determination of the level of specific pathogens, spoilage or indicator micro-organisms.
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